Color	Identification of a protein kinase multigene family of lidentification of a protein kinase multigene family of Dictyostellum discoideum: Molecular cloning and expression of a Dictyostellum discoideum: Molecular cloning and expression of a Prote, Maril. Acad. Sci. 10.5.4. 88, 1115-1119 (1991) Location/Qualifiers
	AUTHORS Maribabu, B. and interpretation of Dictyoste; lum disconting a JOURNAL Proc. Mari. Acad MEDLINE 91142122 FATURES Location in 187 / Source 1 87 / Source CDS <1
Copyright (c) 1993 - 2000 Compugan Ltd. OM nucleic anceleic search, using sw model Run on: May 29, 2002, 09:42:16 ; Seconds Run on: May 29, 2002, 09:42:16 ; Search time 5865,16 Seconds Run on: May 29, 2002, 09:42:16 ; Search time 5865,16 Seconds Run on: May 29, 2002, 09:42:16 ; Search time 5865,16 Seconds Title: Search (s)	13: em_htg_coner: 13: em_htg_louer: 13: em_htg_louer: 14: em_htg_louer: 15: em_htg_louer: 16: em_htg_louer 16: em_htg_louer 17: em_htg_louer 18: em_htg_louer 19: em_htg_louer 1

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BCT 21-SEP-2000
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Gallusser.A. Karl.J. Lill.H., Stahl.P., Krueger.X. and Borgya,A. Method of identifying n-terminal probnp
Patent: WO 0045176-A 03-AUG-2000;
GALLUSSER ANDRES (DE): KARL JOHANN (DE): LILL HELMUT (DE):
STAHL PETER (DE): RRUEGER RERSTIN (DE): BORGYA ANNELIESE (DE);
ROCHE DIAGNOSTICS GRAHH (DE)
Location/Qualifiers
                                                  2 (bases 1 to 96)
Quattro,J.M. and Jones,W.J.
Quattro,J.M. and Jones,W.J.
Direct Submission
Submitted (22-28-1997) Biological Sciences, University of South Carolina, Coker Life Sciences Building, Columbia, SC 29208, USA
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Escherichia.
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Actinopterygian Fishes
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Sequence 3 from Patent WO0045176.
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Paralichthys dentatus lactate dehydrogenase (LDHA) gene, allele
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Eutaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygli, Neopterygli; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygli; Percomorpha; Pleuronectiformes;
Pleuronectoidel; Paralichthyldae; Paralichthys.
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Havelund,S., Halstr.o slashed.m,J., Jonassen,I., Andersen,A.Sloth.and Markussen,J.
Acylated insulin
Patent: US 5750497-A 4 12-MAY-1998;
Location/Qualifiers
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;
/codon_start=1
/codon_start=1
/product=*protein kinase 4*
/protein_id=*AAA33189.1*
/db_xref=*GI:167724*
/translation=*NLIDOYGHIKLTDEGFARRITENTKSMC*
/translation=*NLIDOYGHIKLTDFGFARRITENTKSMC*
/translation=*NLIDOYGHIKLTDFGFARRITENTKSMC*
                                                                                                                                                          Ouery Match 0.6%; Score 29.6; DB 3; Length 87; Best Local Similarity 59.5%; Pred: No. 1.86+04. Med Matches 50; Conservative 0; Mismatches 34; Indels
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Pred. No. 1.7e+05;
0; Mismatches 40; Indels
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AR007403
AR007403.1 GI:3966887
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Quattro, J.M. and Jones, W.J
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AF025984
AF025984.1 GI:2570847
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Best Local Similarity 55.6%;
Matches 50; Conservative (
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18 of 22

Rabit (New Zealand) DNA, clone lambda-charon 4APFK.

Rabit (New Zealand) DNA, clone lambda-charon 4APFK.

Rabit (New Zealand) DNA, clone lambda-charon 4APFK.

Subaryota: Metazoa: Chordata: Crantata: Vertebrata: Euteleostomi: Mammalla: Eutheria: Lagomorpha: Leporidae; Oryctolagus.

E 1 (Nases 1 to 83).

Strench. B. A., Putney, S. D. and Chang, S. N.

The rabbit muscle phosphofroctoxinase gene: Implications for protein structure. Junction and tissue specificity

B 10603

E 8716603

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12 c 26 g 34 t
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/db_xref="taxon:9986"
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Seguence 31 from Patent WO0142445.
AX173377
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/note=*PFK intron R*
13 c 27 g
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phosphofructokinase.
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                                      linear PAT 21-SEP-2000
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Gallusser, A. Karl, J., Lill, H., Stahl, P., Krueger, K. and Borgya, A.
Gallusser, A. Marl, J., Lill, H., Stahl, P., Krueger, K. and Borgya, A.
Hethod of identifying n-terminal probne
Petent: WO 0061376-A 303-MQC-2000;
GALLUSSER ANDELS, (DE): KRUGER KARL JOHANN (DE): LILL HELHUT (DE):
STAHL PETER (DE): KRUGER KERSTIN (DE): BORGYA ANMELIESE (DE):
LOCALED LIAGNOSTICS GMBH (DE)
LOCALED LIAGNOSTICS GMBH (DE)
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Escherichia
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0.5%; Score 25.2; DB 6: Length 99;
Best Local Similarity 54.3%; Pred. No. 2.8e+05;
Matches 51; Conservative 0; Mismatches 43; Indels
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UTHORS Meagher, R.B. and Summers, A.O.
UTLE Hetal resistance sequences and transgenic plants
OURNAL Patent: US 5668394-A 5 16-SEP-1997;
UDRES LOCATION/OURLIfiers
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Sequence 5 from patent US 5668294.
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/db_xref="taxon:562"
19 c 21 g 20 t
                         70 bp
Sequence 3 from Patent WO0345176.
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AX033159.1 GT:10280023
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 9 AR140801/c DEFINITION

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BASE COUNT ORIGIN

AUTHORS TITLE JOURNAL FEATURES

REFERENCE

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Homo sapiens
Eukaryota, Metazoa: Chordata; Craniata; Vertebrata: Euteleostomi;
Eukaryota, Metazoa: Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 73)
Monckton.D.C and Jeffreys,A.J.
Monckton.D.C and Jeffreys,A.J.
Minisatellite 'isoallele' discrimination in pseudohomozygotes by
single molecule PCR and variant repeat mapping
Genomics 11 (2), 465-467 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92120671
GenBank staff at the National Library of Medicine created this entry | NCB1 gibbsq 76509| from the original journal article.
This sequence comes from Figure 2.
Location/Qualifiers
                                                                            1 (bases 1 to 71)
Toothman, P.J., Ringquist, S. and Gold, L.
High affinity TGF. beta. nucleic acid ligands and inhibitors
Patent: US 573424-A 78 24-MAR-1998;
Location/Qualifiers
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/organ1sm="Homo saplens"
/db_xref="taxon:9606"
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0 c
   GI:3939577
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1 (bases 1 to 71)
1 (bases 1 to 71)
10(bases 2 to 71)
11(bases 3 to 71)
12(bases 3 to 71)
13(bases 4 to 71)
14(gh affinity oligonucleotide ligands to growth factors Patent: US 620/816-A 78 27-MAR-2001;
10cation/Qualifiers
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Best Local Similarity 63.3%; Pred. No. 3.5e+05;
Matches 38; Conservative 0; Mismatches 22; Indels
                                                                                                                                                           linear
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Toothman, P.J., Ringquist.S. and Gold, L.
High affinity TCF. beta. nucleic acid ligands
Patent: US 573144-A 78 24-MAR-1998;
Location/Qualifiers
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Sequence 78 from patent US 5731144.
193480
193480.1 GI:3937950
                                                                                                                                                                      Sequence 78 from patent US 5207816.
AR140801
AR140801.1 GI:14483297
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16 c 22 g
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193480/c LOCUS

INV 05-JAN-1994

linear

DNA

dq 86

RESULT 11 195107/c LOCUS DEFINITION ACCESSION

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U92173 51 bp mRNA linear ROD 19-FEB-1998 Mus musculus clone IC3 T cell receptor beta chain mRNA, partial
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Hus musculus.

Eukarous.

Eukarous.

Hammal.

Hammal.

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Lobates
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Johnston,S.L. and Wettstein,P.J.
Direct Submisted (16-MAR-1997) Immunology, Mayo Clinic, 200 1st St S.W.,
Rochester, MN 55905, USA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-minor CTT-1 antigen specific CDR3 region-
/codon_statt-1
/product-T_cell_receptor beta chain*
/proteil_id-*nacoaRRs.1
/db_xre!-G1:2884947*
/translation-*ycrosupparsGMTLVF*
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/strain="5281,6"
/db.xref="taxon:10090"
/clone="1G;"
/cell_type="cytotoxic T lymphocyte"
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by 41 GTATTCCAGATACCTGTCAGATCAATACAGAGATCAAT 2
          , MN 55905, USA
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Job time: 11566 sec
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U92173.1 GI:2894946
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AUTHORS and Harkussen.)

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JOURNAL Patent: US 575049-7 9 12-MAY-1998;

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2 (bases 1 to 98)
3 obases 1 to 98)
Johason Schlitz. Lin. and Engels, W. R.
Johason Schlitz. Lin. and Engels, W. R.
Deleasont Induced interallelic gene conversion of insertions and deletions in Drosophila melanogaster
Whol Cell. Biol. 13, 7006-7018 (1993)
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0.51: Score 24.4; DB 3; Length 98:

Best Local Similarity 56.11; Pred. No. 4.56+05;

Matches 46; Conservative 0; Mismatches 36; Indels 0; Gaps
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Sequence 9 from patent US 5750497.
AR007408
AR007408.1 GI:3966892
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AR007408/c
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AASC6930
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AASC6930
AAC15541
AAT65208
AAX23453
AAX23453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INTR-) INTROGENE BY. (UYLE-) RIJKSUNIY LEIDEN
 WPI: 1997-065462/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09641875-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-DEC-1996.
AAT50934;
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AAT50934
ID AAT5
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(*Linbout alignments)
17574.100 Million cell updates/sec
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Human scretced pro
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Mercurit On reduc
Priner 307-3395 for
GFP Leu(CTG)5 forw
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                                                                                                                                                      1 ctagaagactccccgatga.....ggtttattttaggaaagctc 4990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                1736436 segs, 858457221 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                       ON nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT50934
AAC19445
AAG6400
AAH48689
AAT22086
AAT92244
AAT228594
AAT3346
                                                                                                                                                                           IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                               N_Geneseq_032802:*
                                                                                                                            US-09-676-436-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BB
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Match Length D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 100
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Nucleic acid encoding p53-binding protein - which has homology to mouse Hdm2, for use it cancer research

Score

Result

27.2 26.6 26.6 25.2 25.2 25.2 25.2 25.2

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They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                 AAQ86400 standard; DNA; 100 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94WO-DK00347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94US-0190829
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                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NOVO ) NOVO-NORDISK AS.
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                                                                                                                                                                                                                      203 tgg 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Andersen AS,
Markussen J;
                                                                                                                                                                                                                                                                                                                                                                                             16-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09507931-A.
                                                                                                                                                                                                                                                    12 TGG 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is one of a large number of 5' ESTs derived from manks encoding secreted proteins. No ORF has yet been conclustively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dr primed cDNA libraries. Such ESTs are not well suited for isolating CDNA sequences where longer CDNA sequences have been obtained, the full 5' OTR is rarely included. S. ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length CDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, quene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                    1122 gtatgagggtgatgacacagaaggagaattaaaggagttggaaagtagtacggatgagag 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining CDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                       O; Gaps
                                                                                                                                                                                                                                                                                                  1 gtatgaggtggaagaaacagaagtggtcatnaagtcataccagaagaacagcgatcagga 60
                           The sequences of the 5' region (AAT50934) and 3' region (AAT50935) vere detd. for cDNA clone 1, isolated from a mouse 16-day embryo CDNA library using tumour suppressor p53 as probe. The 5' and 3' regions (AAT50936-37) of another clone were also detd. These sequences showed no significant homology to any known sequence submitted to several databases. A third clone (see also AAT50933) coded for a p53 binding protein designated Mdmx (AAN10206).
                                                                                                                                                                                                    Query Match 0.5%; Score 27.2; DB 18; Length 78; Best Local Similarity 58.1%; Pred. No. 1e+03; Matches 43; Conservative 2; Mismatches 29; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted, protein 5' EST, SEQ ID NO: 23520.
                                                                                                                                                        Sequence 78 BP; 33 A: 9 C: 22 G: 10 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dumas Milne Edwards J, Duclert A, Glordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID 23520; 71pp + CD-ROM; English.
 Disclosure: Fig 2a; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC19445 standard; cDNA; 92 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-FEB-2000; 2000EP-0200610.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                 1182 tgaagaagaacaa, 1195
                                                                                                                                                                                                                                                                                                                                                              61 tgvnghagacaaaa 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI: 2000-500381/45.
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The two subunits of the derivative are covalently connected via disulphide bonds between Cys residues A7/87 and A20/819. The derivative, which may be present as a zinc lon complex, can be used as a fast action freatment for diabetes.
                                                                                                                                                                                                                          Gaps
                                                                                                                                                         21; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human insulin derivative; A-chain; diabetes; zinc ion complex
Alazi PCR primer #128; ss.
                                                                                        Query Match 0.5%; Score 26.6; DB 21; Length 92; Best Local Similarity 57.1%; Pred. No. 1.7e+03; Matches 36; Conservative 6; Mismatches 21; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.5s; Score 26; DB 16; Length 100; Best Local Similarity 55.6%; Pred. No. 2.7e+03; Matches 50; Conservative 0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acylated insulin deriv. which may be present as a Zinc ic complex - is used to treat diabetes and is rapid acting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human insulin derivative Ala21 A-chain PCR primer #128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Havelund S. Jonassen I;
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Sequence 92 BP; 12 A; 9 C; 15 G; 47 T; 9 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 30; 100pp; English.
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This invention describes a novel method to detect N-terminal pro-brain nattiuretic popitide (BMP) in a sample using two antibodies, that recognize different elitopes of the N-terminal pro-BMP. The method can be used for diagnosting heart issufficiency. The recognizant N-terminal pro-BMP is useful as a standard in a method to detect N-terminal pro-BMP is useful as a standard in a method to detect N-terminal pro-BMP is useful as a standard in a method to detect N-terminal pro-BMP is sequence represents a primer used in the cloning of recombinant versiminal pro-BMP in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Obery Match 0.55: Score 25.2; DB 21: Length 70: Best Local Similarity 62.99; Pred: No. 3.7e-03. 3.7e-03. Wetches 39; Conservative 0: Marches 23; Indels 0: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identification of N-terminal pro-brain natriuretic peptide (pro-BNP) using two antibodies that recognize different epitopes of the N-terminal pro-BNP, useful for diagnosis of hear; insufficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene signature: messenyer RNA: mRNA: relative abundance; frequency; human: confing mapping: now-blased library; diagnosis: detection: cell typing: abuncmal cell function: ss.
                                                                                       Brain natriuretic peptide: BNP; primer; human; detection; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Karl J, Lill H, Stahl P, Krueger K, Borgya A, Gallusser A:
                                           Human brain natriuretic peptide N-terminal primer Pro2hum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 70 BP; 10 A; 19 C; 21 G; 20 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT22086 Standard; CONA to mRNA; 89 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1: Page 32: 35pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human gene signature HUMGS03631.
                                                                                                                                                                                                                                                                                                                                                                                                (HOFF ) ROCHE DIAGNOSTICS GMBH.
                                                                                                                                                                                                                                                                                        27-JAN-2000; 2000WO-EP00602.
                                                                                                                                                                                                                                                                                                                                 99DE-1003489
  11-DEC-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-499359/44.
                                                                                                                                                                                                  M0200045176-A2.
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                                                                                                                                                                                                                                                                                                                              29-JAN-1999:
12-MAR-1999;
                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo saptens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W05514772 - A1
                                                                                                                                                                                                                                            03-AUG-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT AAT 22086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel use for sequence variants of the human G-protein betal subunit to predict physiological and pathological pathways in the human body. The invention may be used to detect. detect predisposition for, give a prognosis of, or treat a variety of diseases including high blood pressure, hypertonia, cardiac infarction. Coronary diseases, immunological diseases, asthma, psoriasis, Crohn's disease, collicis ulectors, transplant rejection, mit or supertitia so t. This sequence represents a fragment of the human G-protein Gbetal subunit introm 9 which is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                           Muman: G-protein subunit Geeta3; variant; high blood prossure; asthma; hypertonia; cardiac infarction; coronary disease; heart disease; efrculation disease; abbetes; psychiatric disease; Crohn's disease; tramplodatora disease; portlasis; colitis ulcerosa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of sequence variants of the betal subunit of human G protein to predict, detect, and determine drug targets for diseases including heart, immunological and psychiatric diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        507 ctcagtctcaaagaaaaagacaggagcaaagagacaagaaaaatacgtctgg 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.5%; Score 25.2; DB 22; Length 60; 65.7%; Pred. No. 3.4e+03; ative 0; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                        Human G-protein subunit Obeta3 intron 9 DNA fragment #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 60 BP: 6 A; 11 C: 6 G; 37 T; 0 other;
Disclosure; Page 3; 14pp; German.
                                                                                                                           AAH48689/c
ID AAH48689 standard; DNA; 60 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA71594 standard; DNA; 70 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-JUN-2000; 2000DE-1030945.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-FEB-2000; 2000DE-1004681.
21-FEB-2000; 2000DE-1007587.
                                                                                                                                                                                                                                         19-OCT-2001 (first entry)
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Matches 36: Conservative
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DE10030945-A1. Homo saptens.

AAH48689;

09-AUG-2001.

Siffert W:

AAA71594;

S

RESULT

Query Match

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95US-0427C97

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AA228594
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                                                                                                                                                                                                                         A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 'SG sequences double-stranded DNA) which comprises one of the 7837 'SG sequences double-stranded DNA) which comprises one of the 7837 'SG sequences greated the form and the form the form and form and form and the form and form the form and form and form the GS sequences) as a means of inagnosing abnormal cell function or for recognising different cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0: Gaps
                                                                                                                                                  Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abnormance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Hatch 0.5%; Score 25.2; DB 16; Length 89; Best Local Similarity 62.9%; Pred. No. 4.4e+03; Matches 39; Conservative 0; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Metal ion resistance; mercuric ion reductase; merA; mercury; toxtc heavy metal; transpenic plant; mutagenic; bacterial; transposon; 1701; PCR; 98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mercuric ion reductase merA PCR mutagenesis primer 307-339S.
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 89 BP; 39 A; 8 C; 15 G; 27 T; 0 other;
                                                                                                                                                                                                     Claim 1; Page 1039; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT92244 standard; DNA; 99 BP.
                      94WO-JP01916
                                             93JP-0355504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JAN-1998 (first entry)
                                                                                                      Matsubara K, Okubo K;
                                                                  (MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
                                                                                                                          WPI; 1995-206931/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transposon Tn21
                      11-NOV-1994;
                                             12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4545 gt 4546
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01-JUN-1995
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Organometal: resistance: transcription; translation; regulation; merA: transposon; Inll; merB: mercuric ion reductase; organometrury lysee: ss; transpentc plant; detoxification; metal compound; soil; sediment; primer: aquatic environment; borcemediation; contemination: PCR: amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a PCR mutagenesis primer used to mutagenise the merk coding sequence derived from transposon Tn21, to adapt it for plant expressibility. The nucleic acid molecule produced is useful for producing transgent plants that are resistant to toxic heavy metals (especially mercury) and so can be used remediate and/or revegetate contaminated areas. The bacterial merk gene is derived from the transposon Tn21, which was originally isolated from the Incompatibility Group IncFII resistance plasmid NR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3026 atgtectgactaaatgtgagaytggtagaggtacaagacceaggtgggegacteaaggat 3085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 aagacccagctataggtgaagctgttactgctgcattcgcatggaaggcattgaagtgc 61
                                                                                                                                                                                                                                                                                       DNA encoding mercuric ion reductase in plant-expressible form - for producing transgenic plants resistant to toxic heavy metals
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0.51; Score 25.2; DB 18; Length 99:
Best Local Similarity 54.34; Pred No. 47.2e03;
Matches 51; Conservative 0; Mismatches 43; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Netal resistance sequences for producing transgenic plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 99 BP; 29 A; 21 C; 25 G; 24 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3086 ttgattttctacaagcaattgaacctgcctttat 3119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 gigageatacteaageaagecaagtigectatat 95
                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Column 43-44; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer 307-339S for In21 merA gene.
                                                                       (UYGE-) UNIV GEORGIA RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYGE-) UNIV GEORGIA RES FOUND INC.
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95US-0427097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-0427097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ28594 standard; DNA; 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-DEC-1999 (first entry)
                                                                                                                                               Meagher RB. Summers AO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rugh CL, Meagher RB,
                                                                                                                                                                                                               WPI; 1997-470112/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-579950/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transposon In21.
21 - APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-0CT-1999.
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WP1: 2001-483447/52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a nucleic acid molecule comprising a coding sequence for an organometal resistance protein, which is operably concerned for an organometal resistance protein, which is operably linked downstream of and under the regulatory control of a plant expressible transcription and translation regulatory sequence. The organometal resistance lopen is sepecially the merk gene from the transposon Tall or the E.coli merB gene, mark encodes a metcutic ion reductase and merB encodes a organometrury lyses. The nucleic acid sequences are useful for producing transgenic plants which are capable of efficiently processing mercury. These plants are able to remove or conficient and aquatic environments providing an efficient coll, seduence represents a PCR primer used to amplify the This mercury from soil, seduence represents a PCR primer used to amplify the This mercury and the mutated by random mutagenesis (see AA22884 228589 for mutated sequences) and the mutated sequences are expressed in the transgenic plants of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a primer used to generate a synthetic gfp dene by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3026 atgtcctgactaaatgtgagagtggtagaggtacaagacccaggtgggcgactcaaggat 3085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 aagacccagctataggtgaagctgttactgctgcattlcgcatggaaggcattgaagl.gc 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Determining translational efficiency of codons in cells, comprising introducing synthetic constructs with reporter eness lused in frame tandem repeats of the codon, and measuring expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Green fluorescent protein; GFP; reporter gene; codon utilisation; translational efficiency; protein abundance; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery March

0.54: Score 25.2; DB 20; Length 99:
Best Local Statianity 54.39: Preci No. 47.549; A7.403; Marches 51: Conservative 0; Mismarches 43; Indels (
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 99 BP; 29 A; 21 C; 25 G; 24 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3086 ttgattttctacaagcaattgaacctgcctttat 3119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Column 17-18; 71pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA73946 standard; DNA; 54 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GFP Leu(CTG)5 forward primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JAN-2000; 2000MO-AU00008.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-DEC-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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CC don followed by a stretch of five identical codons was tused in frame codon followed by a stretch of five identical codons was tused in frame immediately upstroam of a 9fp coding sequence to form the synthetic gene. The amplified fragment was cloned into the mammalian expression we coror promain, which contains 8440 oria and the CMY promoter, and was used in each of or determining the translational efficiency of a codon in a cell. The synthetic construct was introduced into COS-1 colls and expression of the reporter porter (orstructs) was made in which the 9fp gene is preceded in frame by a tainfame reporter constructs was made in which the 9fp gene is preceded in frame by a tainfame reporter to constructs was made in which the 9fp gene is preceded in frame by a tainfame reporter to some their constructs was made in which the 9fp gene is preceded to frame by a tainfame report than their corresponding synonymous codons can be identified. These codons may then be used to replace the less preferred codons of a polyhucleochide so that there is higher protein expression within undifferentiated optithelial cells such as COS-1 cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human: foetal liver; yene expression; single exon nucleic acid probe: ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a single exon nucleuc acid probe for measuring human foetal liver. The single exon nucleuc acid probes may be used for predicting measuring and displaying gene expression in samples derived from human fecal liver. The present sequence is a single exon nucleic acid probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; SEG 10 NO 17996; 639pp + sequence listing; English
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0.54; Score 25; DB 21; Length 54;
Best Local Similarity 69:48; Pred. No. 3:6+03;
Matches 34; Conservative 6; Hismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 54 BP: 9 A: 14 C: 20 G: 11 T: 0 other:
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ID ABA69691 standard, DNA; 91 BP.
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26 + MY - 2000: 2000Us-0201456
30 - JUN - 2000: 2000Us-0608400
31 - AUG-2000: 2000US-0234665
21 - SEP-2000: 2000US-0234665
04 - CCT - 2000: 2000CB-0044265
04 - CCT - 2000: 2000CB-0044265
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wlpo.int/pub/published_pct_sequences.
                                                                                                      Sequence 91 BP; 28 A; 19 C; 13 G; 31 T; 0 other;
      8×388
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ö Gaps ·; Length 91; Ouery Match 0.5%: Score 25; DB 22; Length 91.
Best Local Similarity 61.5%; Proci No. 5.1e+03; Indels Matches 40; Conservative 0; Mismatches 25; Indels 3875 agctc 3879 7 ATCTC 3 ò 윩 ò

Human secreted protein 5' EST, SEQ ID NO: 16467. AAC12392 standard; cDNA; 77 BP 06-OCT-2000 (first entry) AAC12392; RESULT 11 AAC12392/c

Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; sa.

Homo sapiens.

EP1033401-AZ.

06-SEP-2000.

21-FEB-2000; 2000EP-0200610

99US-0122487 26-FEB-1999;

(GEST) GENSET

Dumas Milne Edwards J, Duclert A, Glordano

WPI; 2000-500381/45.

New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures

Isolated infectious chimeric parainfluenza virus (PIV), useful in an attenuated vaccine to elicits an immune response against one or more virus(es) sclected from human PIV1 (HPIVI), HPIV2 and HPIV1 -

Example 10; Page 150: 305pp: English.

Claim 1; SEQ ID 16467; 71pp + CD-ROM; English.

The present sequence is one of a large number of 5' ESTs derived from MRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyar RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranalated region (UTR) of the mRNA because they are often obtained from oligo dT primed CDNA libraries. Such ESTs are not well suited for isolating CDNA sequences con a ferrow of the mRNAs and even in those cases where longer CDNA sequences have been obtained. The full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore becaused to obtain full length CDNAs and genomic ONNAs. 5' ESTS are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures they are used to obtain upstream regulatory sequences and to design expression and secretion vectors.

The present sequence for reverse PCR primer for respiratory syncytial viria free present sequence for reverse PCR primer for virus (RSV) A G gene insert is used with the forward PCR primer (AASO6939) in the construction of bowine/humaply3-RSV chimeric virus (SSV) and an invention relating to move infectious.

The sequence is described in an invention relating to move infectious chimeric parathfluenza viruses (PIVS). The virus comprises a major cutience protein (N), and a partial or complete PIV vector background genome. The rotation of more heterologous gene(s) or genome or antigenome combined with one or more heterologous gene(s) or genome or antigenome. The chimeric PIV is useful in an attendated vaccine to elicit an immune response against one or more virus(es) selected from human PIVI, HPIVI), and HIPVI in the chimeric PIV may also elicit a polyspecific immune response against HPIVI may also contain two chimeric PIVs, where the first chimeric PIV elicits an immune response against HPIVI or HPIV2, and where both the first and immune response against HPIVI or HPIV2, and where both the first and immune response against HPIVI or HPIV2 and where both the first and immune response against HPIVI or HPIV2 and wall st he second chimeric PIVs elicit an immune response against HPIVI or HPIV2 are useful as vaccines to parhogen: Chimeric PIVs ellicit an immune response against HPIVI and HPIVI are useful as vaccines to prevent measles and upper or lower respiratory tract infections

Sequence 77 BP; 27 A; 14 C; 15 G; 21 T; 0 other;

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301 gactcagtgggtggatctttgccaaaaalcaattccagatgtggatctcaataagct 360
                       Gaps
                                                                                                                                                                                                                                               Infectious chimeric parainfluenza virus; antigenic determinant; nucleocapsid phosphoprotein; large polymerase; attenuated vacchie; human PIVI; HPIVI; HPIVI; HPIVI; RSY; pathogen; measies; PCR primer; respiratory syncytial virus; respiratory tract infection; bovine; ss.
                                                     14 GACTGTGTGGTGCGTTTGTTTGTTAAAAATATAACTCCCCATTGCTCTCTGGGATAAAGTCT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murphy BR, Collins PL, Schmidt AC, Durbin AP, Skiadopoulos MH;
                       ;
0
0.5%; Score 24.8; DB 21; Length 77; 60.3%; Pred. No. 5.2e+03; Live 0; Mismatches 27; Indels (
                                                                                                                                                                                                                           Reverse PCR primer for RSV A G gene insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                    Human respiratory syncytial virus.
                                                                                                                                         RESULT 12
AASO6930/c
LD AASO6930 standard; DNA: 92 BP.
XX
                                                                                                                                                                                                                                                                                                                                                                                       99US-0170195.
99US-0458813.
99US-0459062.
                                                                                                                                                                                                                                                                                                                                                                   08-DEC-2000; 2000WO-US33293.
                                                                                                                                                                                                        12-SEP-2001 (first entry)
  Ouery Match
Best Local Similarity 60.31
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-356173/37.
                                                                                     361 tacctcag 368
                                                                                                  14 TATCTCAG 7
                                                                                                                                                                                                                                                                                                                         W0200142445-A2.
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10-DEC-1999;
10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                              14-JUN-2001
                                                                                                                                                                                    AAS06930:
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particularly in young children.

Sequence 92 BP; 20 A; 12 C; 26 G; 34 T; 0 other;

ouery Match 0.5%; Score 24.8; OB 22; Length 92; Best Local Similarity 63.3% prod. No 5.9e-02; Indels 0; Caps Matches 38; Conservative 0; Mismatches 22; Indels 0; Caps

AAC11499 standard; cDNA; 94 BP.

06-OCT-2000 (first entry)

AAC11499;

Human secreted protein 5' RST, SEO ID NO: 15574.

Numan: 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.

Homo sapiens.

EP1033401-A2.

06 · SEP · 2000.

21-FEB-2000: 2000EP-0200610.

26-FEB-1999; 99US-0122487.

(GEST) GENSET.

Dumas Milne Edwards J. Duclert A. Giordano J.

New nucleic acid that is a 5' expressed sequence taq (5' EST) for obtaining bobks and genomic Dubbs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures WPI; 2000-500381/45.

Claim 1; SEQ ID 15574; 71pp + CD-RON; English.

The present sequence is one of a large number of 5' ESTs derived from makes conclusived processing secreted proteins. No ORF has yet been conclusively conclusive in conclusively conclusive and conclusively conclusive in the sequence. The sequence the sequence is the sequence sequences as a sequence and in the sequence and in the sequence of the sequence of a sequence and sequence and sequences are not well suited for isolating conk sequences are not well suited for isolating conk sequences of serived from the S' seds and can therefore be conk sequences have been obtained, the full 5' offs is rarely included 5' STS are derived from Minks with intact 5' ends and can therefore be considered to make to obtain full length could and general confidence and sequences are also used in the sequence and sequences and to design expression and secretion vectors.

Sequence 94 BP; 46 A; 9 C; 14 G; 25 T; 0 other;

Query Match 0.5%: Score 24.8; DB 21; Length 94; Best Local Similarity 54.3%: Pred. Mo. 66+03; Gendlarity 54.3%: Oneervalue 0; Mismatches 42; Indels 0; Gaps

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2 gaaaatataaaaalactaaccaaaagaagtcigaqqtaactatggtaatattaaaactcc 61
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1439 acaagetaatqqatqqtteettqeaaqqqea 1476

62 magailteatulaggamataltablumaggem 93

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RESULT 14
AAC15541/c
ID AAC15541 standard: CONA: 94

AAC15541;

06-OCT-2000 (first entry)

Human secreted protein 5' EST, SEQ ID NO: 19616.

Muman: 5' EST; expressed sequence tag: scoreted protein; cDNA isolation; gene therapy; chromosone mapping: ss.

Homo saptens.

EP1033401-A2

06-SEP-2000.

21-FEB-2000; 2000EP-0200610.

59US-0122487 (GEST) GENSET. 26-FEH-1999;

Dumas Milne Edwards J. Duclert A. Giordano J.

WP1; 2000-500381/45.

New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic. forensic, gene therapy and chromosome mapping procedutes

Claim 1; SEO ID 19616; 71pp + CD-ROM; English.

The present sequence is one of a large number of 5' ESTs derived from mixes encoding secreted proteins. Wo ORF Mas yet been conclusively conclusively clearly includent lines have prepared from total human RMAs or polyy-RMAs derived from 30 different tissues. EST concluded human RMAs or polyy-RMAs derived from the Conclusively from the State Lists of the MRA sorb they are often obtained from oligior of primed conk. Internets Such ESTs are not vell suited for isolating conk sequences they are not vell suited for isolating conk sequences they are not vell suited for isolating conk sequences. Both ESTs are not vell suited for isolating conk sequences are derived from makks with intact 5' ends and on therefore be conk sequences have been obtained, the full 5' UTR is rarely included 5' STSTs are derived from makks with intact 5' ends and on therefore be converted from analyse with conks and genomic DNAs. 5' ESTs are also used in dispositic, forensic query therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design

Sequence 94 BP: 35 A: 10 C: 29 G: 16 T: 4 other:

Ouery Match 0.5%; Score 24.8; DB 21; Length 94; Best Local Similarity 59.1%; Pred. Mo. 6e-03. More Set Conservative 2; Wismarches 25; Indels 0; Gaps

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1655 tetace 1660 ô

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The present sequence, a transforming growth factor beta-1 (TGF-beta-1) binding ligand, was identified by Systematic Evolution of Ligands by Exponential enrichment (SELEX). Briefly a candidate mixture of nucleic acids was contacted with TGF-beta-1, and nucleic acids having an increased affinity to TGF-beta-1 partitioned from the remainder of the mixture. The partitioned nucleic acids were then amplified to yield a mixture of nucleic acids enriched for sequences with higher affinity and specificity for binding to requences with higher affinity and specificity for binding to epithelial cell proliferation, or in the diagnosis and treatment of TGF-beta-1 mediated pathological conditions, e.g. fibrocic conditions such as fibroids of the kidney, lung and liver and more acute conditions such as dermal scarring and restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identification of nucleic acid ligands to TGF-beta, PDGF and hKGF using SELEX, used in the diagnosis and treatment of proliferative
                                                                                                                                                        Transforming; growth factor; beta-1; TGF-beta-1; binding ligand; identification; SELEX; anti-mitogenic; inhibition; cell; Systematic Foolution of Ligands by Exponential enrichment; epithelial; proliferation; diagnosis; treatment; fibroids; kidney; lung; liver; dermal scarring; restenosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gold L, Janjic N, Pagratis N, Ringquist S, Toothman PJ;
                                                                                                                               Transforming growth factor beta-1 binding ligand D 11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 15; Page 123; 209pp; English.
RESULT 15
AAT65208/c
ID AAT65208 standard; DNA; 71 BP.
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950S-0458423.
950S-0458424.
950S-0465591.
950S-0479725.
950S-0479725.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NEXS-) NEXSTAR PHARM INC.
                                                                                              10-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-034387/03.
                                                                                                                                                                                                                                                                                              WO9638579-A1.
                                                                                                                                                                                                                                                                                                                                                                                             20-MAR-1996;
02-JUN-1995;
02-JUN-1995;
05-JUN-1995;
07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                30-MAY-1996;
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                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders
                                                               AAT65208;
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Gaps Query Match

O.5%: Score 24.6; DB 18; Length 71;

Best Local Similarity 65.5%; Pred. No. 5.7ev0.3;

Matches 36; Conservative 0; Mismatches 19; Indels 0;

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Search completed: May 29, 2002, 13:05:25 Job time: 9833 sec

Page 1

Title: Perfect score: Sequence: Scoring table:

Run on:

Searched:

Database :

0; Gaps

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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Mammalia: Eutheria: Primates; Catarthini; Hominidae; Homo.

1. (Dases 1 to 71)

RS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NGILOMAI Cancer Institute. Cancer Genome Anatomy Project (CGAP).

Tumor Gene Index

National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Email: cgapbs-remail.nih.gov

Contact: Robert Strausberg, Ph.D.

CDNA Library Preparation: N. Bento Soares, Ph.D.

CDNA Library Preparation: N. Bento Soares, Ph.D.

CDNA Library Arrayed by: Gree Lennon, Ph.D.

CDNA Library Arrayed by: Gree Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

Lond through the I.M.A.G.E. Consortium/LINL at:

Insert Length: 785 Std Error: 0.00

Seq primer: -400P from Gibco

High quality sequence stop: 70.

Location/Qualifiers

Location/Qualifiers
Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte ZNBM), pregnant uterus NBHPU, and fetal heart NBHHPU) were maked, and setal heart NBHHPU) were mixed, and setal heart NBHHPU) were mixed, and setal normal solutreactive hypitodization was used as tracer in a subtractive hypitodization freaction. The driver was POR-amplified CDNAs from pools 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260212-265223, and 484488-489479."
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0.6%; Score 29; DB 9; Length 70;
Best Local Similarity 71.7%; Pred. No. 1.4e+04;
Matches 38; Conservative 6: Mismatches 15; Indels
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Bukaryota: Butherlar Primetes; Catarrhin; Hominidae; Homo.

Hallier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,

Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,

Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylle,

"I. Materaton, R. and Milson, R.

"T. Materaton, R. and Milson, R.

"Mashily-Merck EST Project 1997

Contact: Wilson RR

Washily-Merck EST Project 1997

Contact: Wilson RR

Washington University School of Medicine

Hashington University School of Medicine

144 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Fax: 314 286 1810
        AA490364

aa44c10.rl Soares_NhHWPu_Sl Homo sapiens cDNA clone IMAGE:823794 5' similar to SW:NIM1_NEUCR P48479 PROTEIN KINASE NIM-1;, mRNA
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This clone is available royalty-free through LLNL: contact the
TMAGE Consortium (info@fimage.linl.gov) for further information.
Trace considered overall poor quality
Sossible reversed clone: similarity on wrong strand
Seq primer: -20ml3 rev2 ET from Amerisham
High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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REFERENCE AUTHORS

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FEATURES

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11.0001 Jacob Strongyloides trichosuri ED pAMP vi Chiapelli McGarier Parastrongyloides trichosuri ED pAMP vi Chiapelli HoCarier Parastrongyloides trichosuri cDNA 5', mRNA sequence. B1312285 G1:15001471 EST.
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                                                                                                                                                                                                                                                                                                                     COMA Library Preparation: M. Bento Soarcs, Ph.D., M. Fatima Bonaldo, Ph.D.
Bonaldo, Ph.D.
COMA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Clone distribution: NET-CGAP clone distribution information can be found through the I.M.A.G.E. Consortlum/LLN at:
Way-biol, Inl. gov/bopy/mage/lmage.html
Insert Length: 1558 5td Error: 0.00
Seq primer: 400P from Gibco
High quality sequence stop: 76.
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**McCarter, Clifton.S., Chiapelli, B., Pape, D., Martin, J., Wylie, T.

**Dante, M., Hartra, M., Hillier, L., Kucaba, T., Theising, B., Bovers, P.
                 Homo sapiens
Eukaryota: Wetazoa: Chordata: Craniata; Vertebrata: Euteleostomi;
Mammalia: Butheria: Primates: Catarrhini: Hominidae; Homo.

1 (bases: I to 83)
WCI/MINOS CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.

WALIMINOS CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.

Mational Cancer Institute / Mational Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
Unpublished (1958)
Contact: Robert Strausberg, Ph.D.

Email: cgapbs: Tamali.nlh.gov
Email: cgapbs: Tamali.nlh.gov
Tissue Procurement: David N. Louis, N.D., Myrna R. Rosenfeld M.D.
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O.61, Score 27 8: DB 9: Length 83:
Rest Local Similarity 59:54: Pred No. 38-04:
Matches 47; Conservative 0: Mismatches 32; Indels 0:
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Parastrungyloides tr:chosuri.
Parastrungyloides trichosuri.
Parastrungyloides. Phromadores; Rhabditide:
Panagrolaimoidea: Strongyloididae: Parastrongyloides.
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SOURCE
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DEFINITION 4989409 x1 WCI_CGAP_Brn25 Homo Sapiens CDNA clone TNAGE:2019185 3',
ACCESSION AI360096
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Amphibia: Batzochia: Anura: Mesobatrachia: Pipoideo;
Xenopodinae; Xenopus.
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Kitayama, A., Terasaka,C., Mochii,W., Ueno,N., Shin'i,T. and Kohara
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/clone_iib-*NIBB Mochil normalized Xenopus tailbud
_ibrary*
                       Ouery Match

0.64: Score 28.6: UB 9: Length 71:
Best Local Similarity 64.21: Pred. Mo. 1.78+04.

Matches 4.3: Conservative 0: Mismatches 24: Indels

Matches 4.3: Conservative 0: Mismatches 24: Indels
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Center For Genetic Resource Information
National Institute of Genetics
1111 Tate, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="whole embryo"
/dev_stage="stage 25"
15 a ll c ll g 42 t
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/db_xref-"taxon:8355"
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Location/Qualiflers
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                                                                                                                                                     Wilson, W. The Washington Univ. Nematode EST Project, 1999

Washington Univ. School of Medicine

4444 Forest Park Parkway. Box 8501, St. Louis. WO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1800

Fax: 314 286 1800

Email: estewatson. wustl.edu

The library was constructed by Brandi Chiapelli and Dr. James

McCarter (bchiapel@watson. wustl.edu i jmccarte@watson. wustl.edu)

The library was constructed by Brandi Chiapelli and Dr. James

McCarter (bchiapel@watson. wustl.edu i jmccarte@watson. wustl.edu)

University Genome Sequencing Center St. Louis.

Putative full length read

The vector to vector length is 95

Seq primer: -40RP from Globco.

Seq primer: -40RP from Globco.
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/dev_grage="Free Living"
/lab.host="bH108"
/note="vector: pAMP1 (Gibco): Site_1: Not1; Site_2: Sall:
/note="vector: pAMP1 (Gibco): Site_1: Not1; Site_2: Sall:
/note="vector: pAMP1 (Gibco): Site_1: Not1; Site_2: Sall:
/note="vector: pAMP1 (Gibco): Site_1: Not Dr.
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AA154655
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Leh M., Martin,J., Morris,M., Schallenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvill.R., Ronkoj., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Stoptoe, M., Allen, M., Person, B., Swaller, T., Harvey, M., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
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/Organism="Parastrongyloides trichosuri"
/db_xref="taxon:131310"
/clone_lib="Parastrongyloides trichosuri FL pAMP1 v1
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91 bp mRNA linear EST 17-MAR-1995 yddidio.rl Soares fetal liver spleen lNFLS Homo sapiens cDNA clone IMAGE:112723 5' similar to gb:x56468_rnal 14-3-3 PROTEIN THETA HUMAN); mRNA sequence.
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1 (bases 1 to 91)
1 (bases 1 to 91)
1 (hiller, C., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Riktin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
                                                                                                                                                444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Faxil: mousest watabon. Wustl.edu
This clone is available royalty free through LLNL: contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                           Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seg primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.
Locality sequence stop: 1.
10.000
Waterston.R.
The WashU-HHNI Mouse EST Project
Unpublished (1996) EST Project
Contact: Marra M/Mouse EST Project
WashU-HHNI Mouse EST Project
Washington University School of Medicine?
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15 Carochabditis elegans.
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16 Caenorhabditis elegans.
16 Caenorhabditis elegans.
17 Caenorhabditide: Peloderinae. Caenorhabditis.
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18 Rhabditide: Peloderinae. Caenorhabditis.
18 Chara. T. Wothsah. T. Tabara. H., Watanabe. H., Sugimoto. A., Sano.
18 Chara. T. Wothsah. T. Tabara. M. Watanabe. H., Sugimoto. A., Sano.
18 Chara. P. Wothsah. A.
18 Chara. T. Wothsah.
18 Chara. P. Wothsah.
18 Chara. B. Wothsah.
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/organism-'cenorhabdilis cleqans'
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/clone-'yk2595;
/clone-'yk2595;
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/tissue_type-'whole animal'
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//dev_aloge="20 week-post conception fetus"
//deb_nost="Dhina daylocal"
//deb_nost="Dhina daylocal"
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AJ054186 AM054386.18 GI:3322173
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Bukaryota; Wetzoa: Chordata: Cranlata; Vertebrata; Euteleostomi;

Bukaryota; Wetzoa: Chordata: Cranlata; Vertebrata; Euteleostomi;

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Contact Roberts Strauberg, Ph.D.
Emall: egglebs remail.inlingov
Emals: egglebs remail.inlingov
Rasse Profutement: Honitos Brown, W.D., Elise Kohn, H.D., Michac.
R. Emmert Buck, M.D., Ph.D.
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             The WashU-Merck EST Project
Uppublished (1955)
Contact: Wilson RK
Washington University School of Medicine
(444 forest park Perkway, Box 8501, St. Louis, MO 63108
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/Ob_xeref="Gosto"
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//sex="male"
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/$train="ryB/N"
/db_xref="taxx.n:1009"
/clone="itha="Kol.cCAP_Mam6"
/sex="female="ithilitating ductal carcinoma"
/sex="female="infilitating ductal carcinoma"
/sex=spee="s months"
/lab_host="DB108"
/note="Organ mammary; Vector: pCMV-SPORT6; Site_1: Sall;

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Mammalla: Eutheria: Rodentla: Sclurognathi; Muridae; Murinae; Mus.

1 (Bases 1 tto 81)

1 (Bases 1 tto 81)

Mittonal Institutes of Health, Mammalian Gene Collection (MGC)

Mittonal Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Jeffrey Green M.D.

CONA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CONA Sequencing by: They Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 81.

Location/Qualifiers
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MD mRNA sequence.
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EST3242.1 GI:9816962
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0.5%; Score 26.8; DB 10; Length 100;
Best Local Similarity 55.3%; Pred. No. 5.9e+04;
Matches 52; Conservative 0; Mismatches 42; Indels 0.
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/dev_stage="varied"
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4982 ggaaa 4986

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BF101686 82 bp mRNA linear EST 19-OCT-2000 601753418F1 NCI_CGAP_Maml Mus musculus cDNA clone IMAGE:3980885 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"Organ: mammary: Vector: pCNV-SPORT6: Site_1: SalI; Site_2: NotI: Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH*
                                                                                                                                                                                                                        Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eukaryota, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 82)
NIH-MCG http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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CDNA Library Arrayed by The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
flound through the I.M.A.G.E. Consortium/LLNL at:
http://nmage.lul.gov
Plate: LLAM9177 row: d column: 06
High quality sequence stop: 82.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
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/clone="IMAGE:1980885"
/clone=lib="MCI_CGAP_Maml"
/tissue_rype="tumor, blopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Dmail: cgapbs-r@mail.nlh.gov
Tissue Procurement: Glibert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               house mouse.
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Tunor Gere Index

Outpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Chilstopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Chilstopher Moskaluk, M.D., Ph.D., Michael R.
Contact: Child Preparation: W. Hento Source, Ph.D.
CONA Library Preparation: W. Hento Source, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: KRI-CGR6 Clone distribution information can be found through the I.M.A.G.E. Consortium/LiML at:
Novbelo, Lini,gov/belg/mage/Lingque hull
Insert Length: 820 Sed Error: 0.00
Seq primer: -40ml Fwd Er from Ameraham
High quality sequence stop: 87.
Local England Sequence stop: 87.
Local England Sequence stop: 87.
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Schistosoma manson!
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Strigetidda: Schistosomaloidea: Schistosoma.
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Saber: M. Hanied.M. Elivassaki.M.W. Romoth,M. Ahmed,M. Wohareb
Schistosoma mansoni coMas
Urpublished (1995)
Contact: M.A. Saber: H. Hamled, M.M. Elivassaki, M. Rometh, H. Holareb
H. Holareb. I. fi babaa. S. Memdouh
H. Holareb. I. fi babaa. S. Memdouh
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R93104 STR00038 S. mansoni cONN Schistosche nansoni CDNA clone
SYTENDAMSG0388X 5' end. mRNA sequence.
ACCESSION R93104.1 G1:965458
REXINDRUS R93104.1 G1:965458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone-inAAR.1588653.
/clore_ilb-wci_CGAP.X.dds'
/tlssuc_type-2 pooled tumors (clear cell type).
/lab_host-PH108*
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Imbaba, P.O. 80x 12411, Giza, Egypt.
Per: 202 3128276
Fax: 202 3121167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism-"Homo sapiens"
/db_xref-"taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4936 tydaatttaagaaaa 4951
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AUTHORS
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/actsue_type=_tymph mode*
/dev_atage=*a weeks.
/dev_atage=*a ptimed with a wot I = oligoddT primer.
|Sr_atage=*a ptimed cut with Not I and chood into the Not I and Exposed into the No
Namaalia; Eutheria; Rodentia; Sciurognathi; Huridae; Hurinae; Nus.
1 (bases 1 to 87)
4 Astra, Hillier, L., Allen, M., Bowles, M., Dietrich, M., Dubuque, T.,
Gelsel, S., Worbar, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Mylle, T., Lennon, G., Soares, B., Wilson, R., and
Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA946634 95 bp mRNA linear EST 23-JUL-1998 og38f11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1588653 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nono implems Missions, Chordata, Craniata, Vertebrata, Euteleostomi: Mandalda, Eutheria, Primates, Catarrhini: Mominidee: Homo. to bases 1 to 555 NGT: CGAP http://www.ncbi.nim.nih.gov/nc.cqap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dmail: mousessétéatson, uvuti, dec through (LML); contact the This Clone is available royalty-free through (LML); contact the TMMS Consortium (Info@mages.llnl.gov) for further information. MCI:446148 Seq priner: _28ml]_rev2_ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         metation, M.
The MashU-HHMI Mouse EST Project
Onpublished (1996)
Contact: MashU-HHMI Mouse EST Project
MashU-HHMI Mouse EST Project
MashU-HHMI Mouse EST Project
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 0.5%: Score 26.4; 08.9; Length 87; Best Local Similarity 61.8%; Pred. No. 7 1e-04; Matches 42; Conservative 0; Mismatches 76; Indels Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_"!MAGE:720652" /clone_lib="Soares mouse lymph node NDMLN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            r: -28ml3 rev2 ET from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism-*Mus musculus*/strain-*C57BL/6J*/db_xref-*taxon:10090*
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AA946634.1 GI;3110029
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AA946634/c
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VERSION
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AUTHORS
TITLE
                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
COMNENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
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융

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Email: N-Saber@FRCU.EUN.EG

Seq primer: sk.

Location/Qualifiers

1. 95

Corganism="Schistosoma manson!"

Strain="scyptian"

Strain="scyptian"

Adb_xef="taxon:6183"

Clone="strandbadds038s"

Clone="strandbadds038s"

Alab_bost="e.coll tk Bluel"

Anol: mRNA was purified from adult couples of S. manson!

CDNA was constructed and cloned simultaneously using vector priming with the paluescript II SK+: Site_1: EcoRI: Site_2: CDNA was directionally synthesized from the EcoRI site in the vector to the xhol site in the vector to the xhol site in the strain is in the strain in th
                                                                                                                                                                                                                                                                                                                                source
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ORIGIN
                                                                                                                                                                                                                                          FEATURES
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ö Query Match 0.5%; Score 26.4; DB 10; Jength 95; Best Local Similarity 59.2%; Pred. No. 7.3e+04; Matches 45; Conservative 0; Mismatches 31; Indels 0; Gaps

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701 toadagtogactatgg 716 충염

65 TGAATTTTACCATAG 80

Search completed: May 29, 2002, 11:17:02 Job time: 7404 sec

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Sequence 75, Appl Sequence 75, Appl Sequence 75, Appl Sequence 260, Appl Sequence 99, Appl Sequence 99, Appl Sequence 16, Appl Sequence 5, Appl Sequence 5, Appl Sequence 5, Appl Sequence 10, Appl Sequence 11, Appl Sequence 111, Appl Sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SERE: No. 57504970 NO. 5750497disk of No. 5750497th America, Inc. 1405 Lexington Avenue, 64th Floor New York.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4469 aagaatgaayeelagtagaalulggaellggaadutetettaateactgtatgtaa 4528
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O.St. Stoare 26: DB 1: Longth 100;

Best Local Similarity 55:64: Pred. No. 6.1e+02.

Matches 50: Conservative 0: Mismatches 40; Indels 0: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTE: New YORK
COUNTRY: United States of America
COMPUTER: Injuly-6401
COMPUTER REAGABLE FORM:
MEDIUM TIPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC: NOS/95.005
SOFTWARE: PATENTIN PC: NOS/95.005
SOFTWARE: PATENTIN PC: NOS/95.005
SOFTWARE: PATENTIN PC: NOS/96.002
CUNNENT APPLICATION NOWBER: 1995
CLASSITICATION NOWBER: 1995
ATTORNYY/AGENT THROWATTON:
NAME: LAMBLIS: Ellas J.
RECISTRATION NUMBER: 3985.220-U5
RECISTRATION INFORMATION:
TELEPHONE: 212-867-0123
INFORMATION FOR SEC JD NO: 4:
SECOUNCE CHARACTERISTICS:
LENGTH: 100 hase pairs
TTPE: nucleic acid
SYRPE: nucleic acid
STREE NOW NOW ATTORNY NOW ATTOR
US-08-465-591A-75
US-08-465-594A-75
US-08-6973-124-260
US-08-6014-250
US-08-484-652A-99
US-08-484-552A-99
US-08-61-697-166
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US-08-602-693-23
US-08-602-693-23
US-08-602-693-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Havelund, Svend
APPLICANT: Haistrom, John
APPLICANT: Johnssen, 1b
APPLICANT: Andersen, Assir Sloch
APPLICANT: Markussen, Jan
TITLE OF INVENTION: ACYLATED INSULIN
WINNERS OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MESSUL .
Sequence 4, Application US/08400256 .
Sequence 4, Application US/08400256 .
Fatent No. 5/5/0197 .
GENERAL INFORMATION:
         MOLECULE TYPE: UNA
US-08-400-256-4
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Sequence 68. Appli
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-400-256-4
US-08-427-087-5
US-08-427-087-5
US-08-428-75-85-4
US-08-428-78-75-8
US-08-428-78-75-8
US-08-428-78-8
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US-08-428-8
US-08-438-8
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Naximum Match 100%
Listing first 45 summaries
                                                                                                                                       OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Match Length DB ID
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4990
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Maximum DB seq length: 100
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Perfect score:
Sequence:
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: NO. 60110070 NO. 6011007disk of NO. 6011007th America, Inc. STREET: 405 Lexington Avenue, 64th Floor
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Length 100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Parentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/400,256
FILING DATE: 03-MAR-1995
ATTORNEY/ACENT INFORMATION:
NAME: Lamblis, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3985,220-US
TELECOMUNICATION INFORMATION:
TELECHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4529 tatttacataaagactgtgctgagaagcag 4558
                                                           4529 tattlacataaagactgtgctgagaagcag 4558
                                                                                                                                                                                                                                                                                    APPLICANT: Havelund, Svend
APPLICANT: Halstrom, John
APPLICANT: Jonassen, 1b
APPLICANT: Andersen, Asser Sloth
APPLICANT: Markussen, Jan
TITLE OF INVENTION: ACYLATED INSULIN
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 CAATTGGAAAACTACTGTGCTTAGACGCAG 8
                                                                                                      37 CANTIGGAAACTACTGTGCTTAGACGCAG 8
                                                                                                                                                                                                US-08-975-365-4/c
| Sequence 4, Application US/08975365
| Patent No. 6011007
| GENERAL INFORMATION:
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Patent No. 5668294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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US-08-975-365-4
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CONTRICARY Someware altohard B.
APPLICARY Someware Anne O.
TITLE OF INVENTION: Metal Designance Sequences and
TITLE OF INVENTION: Anne O.
TITLE OF INVENTION: Transport Plants
NUMBER OF SEQUENCES: 30
COMPRESS OF SECUENCES: 30
COMPRESS OF SEQUENCES: 30
COMPRESS OF SEQUENCES: 30
COMPRESS TO SEGUENCES: 30
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| WEDDING TYPE: Flopped to the week of the
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PRIOR APPLICATION NUMBER: 07/711.313

FILTING DATE: 10-100.8136.

FILTING DATE: 10-100.8136.128

FILTING DATE: 11-100.8136.128

FRICK PRICIATION NUMBER: 07/336.128

FRILL ROAD PRICIATION DATA: 07/306.128

FRILL ROAD PRICIATION DATA: 07/306.128

FRILL ROAD PRICIATION NUMBER: 08/11.991

FRILL ROAD PRICIATION NUMBER: 08/3-966

CORREST SAND PRICIATION NUMBER: 08/3-966

FRILL ROAD PRICIATION NUMBER: 08/3-966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-973-124-78/C

Sequence 78, Application US/08973124

Sequence 78, Application US/08973124

SEQUENCE 11 UNCORANTION:
APPLICANT: LARRY GOLD et al.
TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLECTIDE
TITLE OF INVENTION: LIGANDS TO GROWTH
TITLE OF SEQUENCES: 304
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swenson & Bratschun, L.L.C.
STREET: 64.00 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage COMPUTER: TRM COMPALIBLE OPERATING SYSTEM: NS-DOS SOFFWARE: Mordberfect 6.1
CURRAT APPLICATION DATA:
MAPLICATION NUMBER: US/08/973,124
FILING DATE: 11-JUNE-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA: 21-OCTOBER-1992
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEBBER-1993
PRIOR APPLICATION NUMBER: 07/91,473
FILING DATE: 17-AUGUST-1992
ATORNEY/AGENT INFORMATION:
NAME: Diane H. MCCLEATION
TELECHONE: 30 JOHN HORDER: 31-90
TELECHONE: (303) 793-333
TELENOME: 71 DASE PAIRS
TOPOLOGY: 11 DASE
NOLECULE TYPE: DUCLECULE TYPE: DNA
US-08-458-424B-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 536
PRIOR APPLICATION DATA
APPLICATION NUMBER: PCT/US96/08014
FILING DATE: 30-MAY-1996
PRIOR APPLICATION DATA
APPLICATION NUMBER: 084/58,423
FILING DATE: 02-JUNE-1995
PRIOR APPLICATION DATA
FILING DATE: 02-JUNE-195
PRIOR APPLICATION NUMBER: 08/458,424
FILING DATE: 02-JUNE-1955
APPLICATION NUMBER: 08/465,594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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FILLING DATE: 05-JUNE 1995

PRIOR APPLICATION RUNBER: 08465,991

PILLING DATE: 07-JUNE 1995

PRIOR APPLICATION RUNBER: 08449,725

FILLING DATE: 07-JUNE 1995

PRIOR APPLICATION DATA: 08419,725

PRIOR APPLICATION DATA: 08419,725

PRIOR APPLICATION NOTA: 08419,725

PRIOR APPLICATION NOTA: 08419,725

PRIOR APPLICATION NOTA: 08419,893

PRIOR APPLICATION NOTA: 08419

PREERENCY DOCKET NUMBER: 03,215

PREERENCY DOCKET NUMBER: 03,215

PROPOLOGY: Linear CHARLES: 03919

PROPOLOGY: Linear CHARLES: 08419

PROPOLOGY: 19411-1870

PROPOLOGY: Linear CHARLES: 08419

PROPOLOGY: Linear CHARLES: 08419

PROPOLOGY: Linear CHARLES: 08419

PROPOLOGY: 19411-1870

PROPOLOGY:
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us-09-676-436-3.szlm100.rni

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ADDRESSEE: No. 55504970 No. 5750497disk of No. 5750497th America, Inc. 55REET: 405 Lexington Avenue, 64th Floor
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match

10.51: Score 24 6: DB 3: Length 72:
Best Local Similarity 59.21; Prof. Mol. 1.36+03:
Matches 42: Conservative 0: Mismatches 29: Indels 0: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: United States of America
COUNTRY: United States of America
LIP: 10174-6401
COMPUTER: REDGABLE FORM:
COMPUTER: REDGABLE FORM:
COMPUTER: HWW PC COMPACTABLE
COMPUTER: HWW PC COMPACTABLE
COMPUTER: HWW PC COMPACTABLE
COMPACTION STOREM: VO.004400.256
FILING DATE: 03-MAR-1995
CIRRELICATION NUMBER: 03/09/400.256
FILING DATE: 03-MAR-1995
CIRRELICATION NUMBER: 33/29
REFRENCE/COCKET NUMBER: 33/29
REFRENCE/COCKET NUMBER: 33/29
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
US-08-400-256-9/C
Sequence 9, Application US/08400255
Sequence 9, Application US/08400255
September 10-5750497
GENERAL HVORMATION:
APPLICANT: Halstrom John
APPLICANT: Andersen. 15
APPLICANT: Markussen. Asser Sloth
APPLICANT: MARKUSSEN. 49
CVRRESPONDENCE ADDRESS:
ADDRESSENE: No. 575000-
                       TELECOMMUNICATION INFORMATION:
TELEPRONE: 201-347-5800
TELEFAX: 201-343-1684
TELEX: 13521
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTER STICS:
LEMENT: 72 buse pairs
TYPE: NOTELE COLD
STRANDEDNESS: double
TOPOLOGIS: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ 10 NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 100 base pairs TYPE: nucleuc acid TYPE: nucleuc acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3754 atggccatgaa 3764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: Linear HOLECULE TYPE: DNA US-08-400-256-9
                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linea NOLECULE TYPE: CD HYPOTHETICAL: NO US-09-100-664A-5
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11: Score 24.6; DB 5; Length 71:
Best Local Similarity 65.5; Preel No. 12e40;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/09100664A
Farent No. 6057129
FAREAL INCORACTION:
APPLICART: VOUNG, MICHAEL W
APPLICART: RLOSS, BRIAN
APPLICART: RLOSS, BRIAN
APPLICART: RLOSS, BRIAN
APPLICART: RLOSS BRIAN
APPLICART: RLOSS, BRIAN
APPLICART: RLOSS BRIAN
APPLICART: ALMORETICAL APPREOF
STREET: All MacKensack Avenue, 4th Floor
STREET: 411 MacKensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WEDUNT TREE FLOPPY GISK
COMPUTER: ISA FC compatible
COMPUTER: ISA FC compatible
COMPUTER: ISA FC compatible
COMPUTER: ParentIn Release #1.0, Version #1.30
CURRENT APPLICATION AND A.

CURRENT APPLICATION AND A.

FILING DATE: 19-JUN-1998
CLASSIFICATION: 415
ATTORNEY AGENT INPORANTION:
NAME: JACKAON ESQ., DAVIG A.

REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,594
FILING DATE: 05-10NE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/45,591
FILING DATE: 05-10NE-1995
FILING DATE: 07-20NE-1995
FILING DATE: 07-30NE-1995
FILING DATE: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New Jersey
COUNTRY: USA
EIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 411 Hack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
US-09-100-664A-5
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APPLICANT: SAVETION CART Palco
APPLICANT: Sharon J. Keeler
APPLICANT: Sharon J. Keeler
APPLICANT: Sharon J. Keeler
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containin
UNIMER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1120 gagtatgagggtgatgacacagaaggagaattaaaggagttggaaagtagtacggatgag 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /function= "synthetic storage protein /product= "protein" /gene= "ssp" /standard_name= "5.11.11.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.5%; Score 24: DB 1; Length 97; Best Local Similarity 58.3%; Pred. No. 2.2e+03; Matches 42; Conservative 0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                    ADDRESSEE: E.I. du Pont de Nemours and Company
STREET: 107 Market Street
CITY: Hilmington
STATE: Delaware
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMFUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: MICROSOFT Word, 4.0
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NOMBER: 07/743,006
FILING DATE: 9 ANGUET 1991
ATTORNEY-AGENT INFORMATION:
NAME: LINGA AXAMETLY FLOYD
REGISTRATION UNBER: 33,692
REFERENCE/DOCKET NUMBER: 38-692
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BB-1031
                 RESULT 12
US-08-182-175A-54
; Sequence 54, Application US/08182175A
; Patent No. 555923
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (302) 992-4929
TELEFAX: (302) 892-7949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 83420
INFORMATION FOR SEO ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 97 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN: E. COLI
CELL TYPE: DH5 alpha
IMMEDIATE SOURCE:
CLONE: 92-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1180 agtgaagaagaa 1191
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OTHER INFORMATION:
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Havelund, Svend
APPLICANT: Halstrom, John
APPLICANT: Johnssen, John
APPLICANT: Andersen, Asser Sioth
APPLICANT: Markussen, Asser Sioth
APPLICANT: Markussen, Jan
TITLE OF INVENTION: ACYLATED INSULIN
MUNBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 60110070 No. 6011007disk of No. 6011007th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
                                                                                          4469 aagaatgaageetagtagaatatggaettggaaaattetettaateactaetgtatgtaa 4528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 AAGTCTGACGACGACGCTAAGGGTATCGTTGAACAATGTTGTACTTGTACTTGTATGTTGTAC 38
                                               Gaps
                                                                                                                                    97 AAGICTGACGACGCTAAGGGTATCGITGAACAATGITGTACTICTAICTGTTCTITGTAC 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.5%; Score 24.4; DB 3; Length 100; Best Local Similarity 54.4%; Pred. No. 1.7e+03; Matches 49; Conservative 0; Mismatches 41; Indels
Query Match 0.5%; Score 24.4; DB 1; Length 100; Best Local Similarity 54.4%; Pred. No. 1.7e+03; Matches 49; Conservative 0; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New York
COUNTRY: United States of America
IIP: 10114-6401
COMPUTER READABLE FORM:
WEDION TYPE: Floppy disk
COMPUTER: BH PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RELIAG DATE:
FLLING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 02 08/400,256
FILING DATE: 03-MAR-1995
ATTORNEY AGENT INFORMATION:
NAME: Lamblits, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/OCCKET NUMBER: 33,728
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy 4529 tatttacataaagactgtgctgagaagcag 4558
                                                                                                                                                                                                             RESULT 11
US-08-975-365-9/c
; Sequence 9, Application US/08975365
; Patent No. 6011007
; CENERAL INFORMATION:
RAVELUNG, Svend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 100 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  us-08-975-365-9
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RESULT 14
PGFSULT 14
PGF1-54
PGT-0452-6412-54
PGGBREAL INFORMATION:
CENERAL INFORMATION:
APPLICANT: Sharow J. Keeler
APPLICANT: Annow J. Keeler
APPLICANT: Jane A. Rice
TITLE OF INVENTION: Spribetic Storage Proteins with Defined Structure Containin
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: E.1. du Pont de Nemours and Company
STREET: 1007 Market Structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="synthetic storage protein
/product="protein"
/gene="ssp"
/standard.name="5.11.11.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 0.51: Score 24: UB 5: Length 97: Best Local Similarity 58:34: Pred: No. 2.2e+73: Marches 42: Conservative U: Mismetches 30: Indels
                                                                                                                                                                                                                                                                                                                                              STATE: Deladore
COMPRY: USA
ZIP: 19896
COMPUTER REALABLE FORM:
MEDIUM TYPE: FLOPPY DISX
COMPUTER: Macintosh
COMPUTER: Macintosh
COMPUTER: Macintosh
COMPUTER: Macintosh
SOFTWARE: Macintosh
SOFTWARE: Macintosh
SOFTWARE: Macintosh
SOFTWARE: Macintosh
TILNG-DATION UNBARE: SOFTWARE
FLING-DATION UNBARE: 30
PRIOR RAPLICATION DATA
SPELICATION MADER: 30
PRIOR RAPLICATION WHORER: 07/43,006
FLITHG DATE: 9 AUGUST 1991
NAWE: LANGA Axamethy Floyd
NAWE: LANGA Axamethy Floyd
REGISTRATION UNBER: 31.692
REFERENCE/DCCKET NUMBER: 38.1031
FRILCOMMUNICATION: NOTALION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (302) 992-4929
TELLERA: (302) 892-7949
TELER: 83420
TELER: 83420
SEQUENCE CHARACTERISTICS:
LENGTH: 97 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN: E. coll
CELL TYPE: DH5 alpha
IMMEDIATE SOURCE:
CLONE: 92-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MARÍARY COS
LOCATION: 2 08
OTHER INFORMATION: /
OTHER INFORMATION: /
OTHER INFORMATION: /
PCT-US92.06412-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1180 agtgaagaag1191
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                                                                                                                                                                                                                                                                                                            Wilmington
Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery March 0.54; Score 24; DB 1; Length 97; Best Local Similarity 58.34; Pred. NO. 2.2e-03; Marches 42; Conservative 0; Mismatches 30; Indels
                                                                                                   APPLICANT: OUPDAY
APPLICANT: COMPANY
TITLE OF INVENTION: HETHOSE FOR INCREASING
TITLE OF INVENTION: METHOSE FOR INCREASING
TITLE OF INVENTION: INCREASING THE LISH WE
TITLE OF INVENTION: METHOSE FOR INCREASING
TITLE OF INVENTION: METHOSE FOR INCREASING
TITLE OF INVENTION: OF THE SEEDS OF PLANTS
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
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/product- protein
/gene - Ssp*
/standard_name-
'5.11.11.5*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-OSC/MS-TOS
SOFTMARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA.
APPLICATION NUMBER: US/08/174,633A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 800
ATTORNEY AGENT INFORMATION:
NAME: BABBARA C. SIECELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: 589-1037-C
TELECOMMUNICATION HIPORMATION:
TELECHNOME: 302-992-4931
                                                                                                                                                                                                                                                                                                   ADDRESSEE: E. I. DU POHT DE NEMOURS
ADDRESSEE: AND COMPANY
STREET: 1007 MARKET STREET
CITT: WILMINGTON
ESULT 13
US-08-414-633A-63
: Sequence 63: Application US/08474633A
: Patent No. 577861
: GENERAL INFORMATION:
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LENGTH: LENGTH: OUGLEC CHARACTERISTICS:
TYPE: nucleic cold
STRANDEDNESS: double
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MOLECULE TYPE: DNA (genor
ORIGINAL SOURCE:
STRAIN: E. COLL
CELL TYPE: DHS Alpha
IMMEDIATE SOURCE:
CLONE: 97-2
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
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LOCATION: 2..88
OTHER INFORMATION: /
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REBULT 15

GUS-D8-67-15A-8

(S-D8-67-15A-8

Sequence 8, Application US/08672158A

FARENT. Workwarton

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APPLICATT: Shery Thompson

TILLE OF INTERNATION

APPLICATION

APPLICATION

STREET: AND ACCOUNTRY: USA

CONTRY: Work TON

STREET: AND ACCOUNTRY: USA

LIN CONTRY: USA

CONTRY: USA

LONGWITHE: PLOPPY disk

CONTRY: USA

LONGWITHE: PLOPPY disk

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CONTRY: USA

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CONTRY: USA

CONTRY: USA

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FILING DATE: TO-102/M2: DOS

CURRENT APPLICATION NOTHS: 34.086

FILING DATE: 212-867-0123

TELECHONE: 312-867-0123

TELECHONE: 312-867-0123

TELECHONE: 312-867-0123

TELECHONE: AS BOD ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: Babe Dails

TOPOLOGY: Lincer

TOPOLOGY: Lincer
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Search completed: May 29, 2002, 12:56:56 Job time: 9665 sec

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# C4 M # 4	en op o		1221 0000		8 6 6 6 7	ផន	ក្នុក ប	0 0 0	3 T S		38.35		0 U U		4 5			DOIDDKD	DEFINITION	VERSION	SOURCE	AUTHORS TITLE	JOURNAL	FEATURES		CDS
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen 1.td.	OM nucleic - nucleic search, using sw model	Num on: May 29, 2002, 09:42:16; Seerch time 5865,16 Seconds (without alignments) 17804.019 Million cell updates/sec	Title: US-09-676-436-3 Perfect score: 4990 Sequence: 1 ctagasgactctccgatgagctttatttaggaaagctc 4990	Scoring table: IDENTITY NOC Gapex: 1.0	Searched: 1797656 seqs, 10463268293 residues	Total number of hits satisfying chosen parameters: 843946	Ninimum DB seq length: 0 Meximum DB seq length: 100	Post-processing: Minimum Match Os Maximum Maxi	Database : GenEmbl:• 1: qb.ba:• 2: qb.ba:• 2: qb.bte:•	3: 95_n:		7: gb_ph:* 8: gb_ph:*	9: 9D_pr: # 10: 9D_pr: #	12: 90_89:* 13: 9b_un:*		17: em_hum:• 18: em_hum:•	13: eec_art. 20:				28: eq_un:+ 29: en_v1:+	32: eq.htgocher: 33: eq.htgo_inv:	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the rotal acore distribution.	SUMMARIES	Result Query	No. Score Match Length DB 1D Description

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Actinoperation in unpublished

E 2 (bases 1 to 96)

RS Quattro.J.M. and Jones.M.J.

Direct Submisser

NAL Submitted (22-SEP-1997) Biological Sciences, University of South Carolina, Coker Life Sciences Building, Columbia, SC 29208, USA

(ES Location/Qualifiers 1 to 96

//Organism="Paralichthys dentatus"

//db_xref="taxon:66718"
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Gallusser.A., Karl,J., Lill,H., Stahl,P., Krueger,K. and Borgya,A. Method of identifying n-terminal probnp
Patent: Wo 0045176-A 03-AUG-2000;
GALLUSSER ANDREAS (DE); KARL JOHANN (DE); LILL HELMUT (DE);
STAHL PETER (DE): RRUEGER KERSTIN (DE); BORGYA ANNELIESE (DE);
ROCHE DIAGNOSTICS (MBHH (DE)
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Amplification Primers That Target Locus-Specific Introns in Actinopterygian Fishes
                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 0.5%; Score 25.4; DB 5; Length 96: Rest Local Similarity 64.4%; Pred. No. 2.4e+05: Matches 38; Conservative 0; Mismatches 21; Indels
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/allele="PdLDHA2"
1. .96
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/db_xref="taxon:562"
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Sequence 3 from Patent WO0045176.
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AX033167.1 GI:10280029
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Peralicithys dentatus
Eukaryota; Metazoa: Chordata: Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa: Chordata: Craniata; Vertebrata; Buteleostomi;
Actinopterygii, Meopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha: Acanthopterygii; Percomorpha: Pleuronectiformes;
Pleuronectoidei; Paralichthyidae; Paralichthys.
I (bases 1 to 96)
Quattro,J.M. and Jones,W.J.
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1 (bases 1 to 100)

1 (bases 1 to 100)

Havelund, S., Halstr. o slashed.m.J., Jonassen, E., Andersen, A. Sloth.

Havelund, S., Halstr. o slashed.m.J., Jonassen, E., Andersen, A. Sloth.

Anylated insulin

Raylated insulin

Patent: US 5750497-A 4 12-MAY-1998;

Location/Qualifiers

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   /codon_start=1
/product=*protein xinase 4*
/product=*protein xinase 4*
/protein_id=*aAx33189.1*
/db_xref="GT:167724"
/translation="NLIDOYGHIKLTDEGFARRITENTKSMC"
/ 1 2 c 1 1 9
                                                                                                                                                       Query Match 0.6%; Score 29.6; DB 3; Length 87; Best Local Similarity 59.5%; Pred. No. 1.8e+04; Matches 50; Conservative 0; Mismatches 34; Indels
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Sequence 4 from patent US 5750497.
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AR007403.1 GI:3966887
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22 c 23 a
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SOURCE OFFICE CONSTRUCT.

ORGANISM synthetic construct.

ORGANISM synthetic construct.

ORGANISM synthetic construct.

ALTHORS WITHOUT N. COL'INS.P. L., Schmidt, A.C., Durbln.A.F.,

ALTHORS Skladopoulos. M. H. and Tau.T.

TITLE Use of recombinant parainfilments virines (plvs) as vectors to proceed against infection and disease caused by prv and other human pathosens and other human pathosens.

JOURNAL Parent: MO 0142445-A 31 14-3UN-2001;

PRAIURES CACACLON/OUBLIFIERS

LACALLON CONTROLLED TO THE CONTROLLED TO TH
Rabbit muscle phosphofructokinase gene, exon 18.
HI4473 J 02702
H14473 J G 1 155622
H0473 L G 1 155622
H0698botructokinase.
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                                                                                                                                                                                                                                                                                                                                                                                          Enlaryonary Milazoa: Chordata: Craniata: Vertebrata: Enteleostomi; Hammalia: Eutheria: Lagomorpha: Laporidae: Orycrolagus.
1 (bases 1.0 0.3)
1. (b
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Location/Qualifiers
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/db_xref="taxon:33630"
/otc="Reverse primer for MSV A G gene insert"
12 c 26 g 34 t
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Oryctolagus cuniculus
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Best Local Similarity 61.5%; Pced. No. 3.1k+05;
Matches 46; Conservative 0; Mismatches 25; Indels
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AX173377 AX17489152
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/note="PFK introm R"
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16. 77
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                                                                                     linear PAT 21-SEP-2000
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Escherichia.
1 (bases 1 to 70)
Gallusser 1 to 70)
Gallusser Anni 1, Lill.H., Stahl.P., Krucger.K. and Borgya.A.
Wethod of identifying n-terminal probap
Petent: WO 043176.A.3 03-ADG-2000;
GALLUSSER ANDREAS (DE) : KARL JOHANN (DE) : LILL HELMUT (DE) ;
STANL PETER (DE) : KRUEGER KENSTIN (DE) : BORGYA ANNELIESE (DE) ;
ROCHE DIAGNOSTICS GRBH (DE)
LOCATION/QUALIFIES
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Dy Andaccaccacctractaanactglacaccaritacaccaritacacce 61

2 Andaccaccacctractacaccaritacaccaritacaccaritacacce 61
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6.51: Score 25.2; DB 6: Length 99;

Feet Local Similarity 54.34; Pred: No. 2.88+05;

Matches 51; Conservative 0; Mismatches 43; Indels 0; Gaps
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0.54; Score 25.2; DB 6; Length 7D;

Bast Local Similarity 62.99; Pered Mo. 2.78+05;

Matches 39; Connervative 0; Mismatches 23; Indels 0; Gaps
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AUTHORS Neagher, R. B. and Summers, A.O.
TITLE Metal resistance sequences and transgenic plants
JOURNAL Patent: US 5668294-A 5 16-SEP-1997;
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/db_xref="taxon:562"
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Sequence 1 from Patent W00045176.
AX033159.1 GI:10280023
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DISS (A) [hypervariable minisatellite MS32] [human, individual MACH, Genomic, 73 nt].
$76509
$75509.1 GI:243382
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1 (Dases 1 to 73)
Monokton, DG; and Jeffreys, A.J.
Minisatallite 'Isoallele' discrimination in pseudohomozygotes by single molecule PCR and variant repeat mapping Genomics 11 (2), 465-467 (1991)
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                                                                                                                           1 (bases 1 to 71)
Toothmab, P.J., Ringquist.S. and Gold, L.
High affinity TSF. beta nucleic acid ligands and Inhibitors
Patent: US 571424 A 78 24 WAR-1998;
Location/Qualifiers
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    . 73
    /crganism-"Homo sapiens"
    /db_xref-"taxon:9606"

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/allale="A"
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  GI:3939577
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Obside 1, Janific M. and Pagratis.N.
High affinity oligonuclectide ligands to growth factors
Patent: US 6207816-A 78 27-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.5%; Score 24.6; DB 6: Length 71; Best Local Similarity 65.5%; Pred. No. 3.9e+05; Matches 36; Conservative 0; Mismatches 19; Indels
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Best Local Similarity 63.3%; Pred. No. 3.5e+05;
Matches 38; Conservative 0; Mismatches 22; Indels
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Toothman, P.J., Ringquist, S. and Gold, L. Toothman, P.J., Ringquist, S. and Gold, L. High affinity TGF beta. nucleic acid ligands patent: US 5/31144-A 78 24-MAR-1998;
Location/Qualifiers
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193480.1 GI:3937950
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Sequence 78 from patent US 5731424.
195107
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U92173 51 bp mRNA linear ROD :9-FEB-1998 Mus muscalus clone 103 T cell receptor beta chain mRNA, partial
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Johnston: S. L. and Hettstein. P. J.
T. cell croceptor diversity in CTLs specific for the CTT-1 and CTT-2 minor Histocompactbility antiques.
J. Immunol. 159 (6). 2606-2515 (1997).
(bases 1 to 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Johnston, S.L., and Wettmieln, P.J.
Direct Submission
Submitted (16-MRR-1997) Immunology, Mayo Clinic, 200 lst St S.W.,
Rochester, MN 55905, USA
Rochester, MN 55005, USA
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/codon_gitair=1
/product.*T cell receptor beta chain"
/product.*T cell receptor beta chain"
/protein_id="Anfo2878.1"
/db_xref="GI:289497"
/translation="YCTCSOPDMYSGNILYF"
12 a is c il g is t
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C.54: Score 24: DB 10: Length 51:
Ped No. 9: Se-orb
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Matches 30: Conservative G: Wismatches 10: Indels
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/strain="C5781/5"
/db_xrai="taxon:10090"
/cione="10" cylotoxic T lymphocyte"
/cell_type="cylotoxic T lymphocyte"
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U92173.1 GI:2891946
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Mus musculus
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ION Drosophila melanogaster DNA sequence, complete insertion sequence.

CN 120950.

120950.1 GT:304832

IS sequence.

Drosophila melanogaster (individual_isolate 820.3) DNA.

ENTARYOTES MetaCoal Arthropoda: Trachela: Hexapoda: insecta: Pteryotes MetaCoal Arthropoda: Trachela: Hexapoda: Insecta: Pteryotes MetaCoal Arthropoda: Trachela: Hexapoda: Insecta: CE I (bases 1 to 9)

FS Engels.M.R. and Johnson-Schlitz.D.M.

Deletion white allele. Transposses-induced derivative of white allele.
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O.5%; Score 24.4; DB 6; Length 100;
Best Local Similarity 54.4%; Pred. Mo.4.5e-65;
Matches 49; Conservative 0; Missatches 41; Indels 0; Gaps C;
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1 (Dages 1 to 100)
and Markassen, 1. Andersen. A. S. oth. and S. S. oth. A. S. S. oth. and S. S. oth.
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2 (bases 1 to 39)
3 (bases 1 to 39)
4 (bases - 1 to 30)
Petenson-Schitz.D.M. and Engels, K. R.
Petenson-Induced interallelle gene conversion of insertions and detections in Drosophita melanogaster
Mol. Cell. Biol. 13, 7006-7018 (1993)
94019372
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1 Marchacaccaraagcaracaccaracacacaracacactroractatratactata 38
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Sequence 9 from patent US 5750497.
ARGU7408.1 GI:3966892
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	OM nucleic - nucleic search, using sw model Run on: Hay 29, 2002, 10:21:32 : Search time 487 5 Seconds	17574 160 Million cell (MILLON 496) 17574 4990	Sequence: I ctagaagactccccgatgaggtttatttaggaaagctc 4990 Scoring table: IDENTITY_NUC Gapop.10.0 , Gapext 1.0	1736436 seqs, 858457271 residues	TOCAL number of hits satisfying chosen parameters: 2045005 Winimum DB seq length: 0 Maximum DB seq length: 100	Post-processing: Minimum Match 00 Maximum Match 1000 Listing first 45 summaries	N_Jenceseq_013801:* A_STOSI_Vegetar_Lyfencecy_(geneseqn.emb]/AA1980.DAT:* A_STOSI_Vegetar_Lyfencecy_(geneseqn.emb_I/AA1981.DAT:* A_STOSI_Vegetar_Lyfencecy_(geneseqn.emb_I/AA1981.DAT:* A_STOSI_Vegetar_Lyfencecy_(geneseqn.emb_I/AA1882.DAT:* A_STOSI_Vegetar_Lyfencecy_(g	8: \\$1051/999data/yeneseq/qeneseq-nemb./his/981.wh. 9: \\$1051/999data/yeneseq/qeneseq-nemb./his/981.wh. 10: \\$1051/999data/yeneseq/geneseq-nemb./his/981.bxT:* 11: \\$1051/999data/yeneseq/geneseq-nemb./his/1991.bxT:* 12: \\$1051/999data/yeneseq/geneseq-nemb./his/991.bxT:* 13: \\$1051/999data/yeneseq/geneseq-nemb./his/991.bxT:* 14: \\$1051/999data/yeneseq-nemb./his/991.bxT:* 15: \\$1051/999data/yeneseq-nemb./his/991.bxT:* 16: \\$1051/999data/yeneseq-nemb./his/991.bxT:* 17: \\$1051/999data/yeneseq-nemb./his/995.bxT:* 18: \\$1051/999data/yeneseq-nemb./his/995.bxT:* 19: \\$1051/999data/yeneseq-nemb./his/995.bxT:* 19: \\$1051/999data/yeneseq-nemb./his/996.bxT:* 19: \\$1051/999data/yeneseq-nemb./his/996.bxT:*	20: /SIDSJ/gogddta/geneseg/geneseg-n-embl/kh1999.bur: • 21: /SIDSJ/gogddta/geneseg/genesegn-embl/kh1999.bur: • 21: /SIDSJ/gogddta/geneseg/genesegn-embl/kh200b.bur: • 21: /SIDSJ/gogddta/geneseg/genesegn-embl/kh200b.bur: • 21: /SIDSJ/gogddta/geneseg/genesegn-embl/kh200b.bur: • 24: /SIDSJ/gogdta/geneseg/genesegn-embl/kh200lB.ont: • 24: /SIDSJ/gogdta/geneseg/genesegn-embl/kh200lB.ont: • 24: /SIDSJ/gogdta/genesegn-embl/kh200lB.ont: • 24: /SIDSJ/gogdta/genesegy/genesegn-embl/kh200lB.ont: • 24: /SIDSJ/gogdta/genesegn-embl/genesegn-embl/kh200lB.ont: • 24: /SIDSJ/gogdta/genesegn-embl/genese	SCORE WATCH LENGTH DB 1D	1 27.2 0.5 78 18 AAT50934 Mouse p53-recognit c 2 26.6 0.5 78 18 AAX79945 Hugan secretical processor c 3 26.0 0.5 100 16 AAX7945 Hugan secretical processor c 4 25.2 0.5 0.0 16 AAX7894 Hugan secretical derivation of the control of th

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The present sequence is one of a large number of 5' ESTs derived from manya encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyar RNAs derived from 30 different Lisaucs. EST sequences usually correspond mainly to the 3' untranalated region (UTR) of the mNNA because thay are often obtained from oligo-dy primed cDNA identived from the STs are not vell suited for isolating cDNA sequences con a sequence have been obtained, the full 5' OTR is rarely included. ESTS are derived from mRNAs with included. S' ESTS are derived from mRNAs and genomic DNAs. 5' ESTS are also used used to obtain full length cDNAs and genomic DNAs. 5' ESTS are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruman: 5' EST; expressed sequence tag; sacreted protein; cDNA isolation;
gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                 1122 gtatgagggtgatgacacagaaggagtattaaaggagttiggaaagtagtacggatgagag 1181
                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                         The sequences of the 5' region (AAT50934) and 3' region (AAT50935) were deter. For const. clone 1, stackted from a mouse 16-day embryo. CDNA library using tumour suppressor p53 as probe. The 5' and 3' regions (AAT50936-37) of another clone were also detd. These sequences showed no significant homology to any known sequence submitted to several detabases. A third clone (see also AAT50933) coded for a p53 binding protein designated Ndmx (AAM10206).
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                                                                                                                                                                                                                                                             Query Match 0.5%; Score 27.2; DB 18; Leagth 78; Best Local Similarity 58.1%; Pred. No. 18+03; Matches 43; Conservative 2; Mismatches 29; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted, protein 5' EST, SEQ ID NO: 23520.
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                                                                                                                                                                                                      Sequence 78 BP; 33 A: 9 C; 22 G; 10 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID 23520; 71pp + CD-ROM; English.
Disclosure; Fig 2a; 30pp; English.
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                                                                                                                                                          143 mannatqaatgcaccaaatcagcctccacataaagacactggmanncagtggagaatg 202
                                                                                                                            Caps
                                                                                                                                                                                They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
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Alazi PCR primer #128; ss.
                                                                                             Length 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Owary Match 0.5%, Score 26; DB 16; Length 100; Best Local Similarity 55:6%; Pred: No. 27+643; Matches 50; Conservative 0; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acylated insulin deriv. which may be present as a fine lon complex - is used to treat diabetes and is rapid acting.
                                                                                           Query Match 0.5%; Score 26.6; DB 21; Length 9
Best Local Similarity 57.1%; Pred. No. 1.7e+03;
Matches 36; Conservative 6; Mismatches 21; Indels
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                                               Sequence 92 BP: 12 A: 9 C; 15 G; 47 T: 9 other;
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                                                                                                                                                                                                                                                                                                                                 AAQ86400 standard; DNA; 100 BP
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94US-0190829
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Identification of N'Esminal pro-brain natifuratic paptide (pro-BNP) insing two antibodies that recognize different aptiopss of line N'ereminal pro-BNP, useful for diagnosts of best insufficiency.
                                                       Brain natibrotic peptide: BNP, primer; human; detection; epitope;
heart; ss.
                                                                                                                                                                                                                                                                                          Karl J, Lill H, Stahl P. Krueger K, Borgya A, Gallusser A:
                             Human brain ratriaretic peptide N-terminal primer Pro2hum.
                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 32: 35pp. German
                                                                                                                                                                                                                                                              (HOFF ) ROCHE DIAGNOSTICS GMBH.
                                                                                                                                                                                          27-JAN-2000; 2000WO-EP00632.
                                                                                                                                                                                                                     29-JAN-1999: 99DE-1003439.
 11-DEC-2000 (tirst entry)
                                                                                                                                                                                                                                                                                                                         WPT: 2000-499359/44.
                                                                                                                                  WO200045176-A2
                                                                                                   Homo saptems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1838 tg 1839
                                                                                                                                                              03-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 Ly 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT22086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel use for sequence variants of the human particular bytesion being about to practice physiological and pathological parthways in the human body. The invention may be used to detect, delicit performantion for, give a proposis of, or treat to variety of diseases including high blood pressure, hypertonia, cardiac inferction, coronary diseases, immunological diseases, atthmat, psort or circulation diseases, otheres, psychiatric diseases, immunological diseases, atthma, psort and psychiatric collits ulceroas, transplant rejection WIY or Hepatitis B or C. This including high diseases in the puman G-protein Obetal subunit income switch and asset to inclusive the method of the Invention.
                                                                                                                                                                                                                Human: G-protein subunit Gbetal; variant; high blood pressure; asthma, hyportoola; cardiac infarction; coronary disease; heart disease; triculation disease; dabetes; psychiatric disease; Crohn's disease; transplant rejection; da.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use of sequence variants of the besi subunit of human G proLein ro
predict, idetect, and determine drug targets for diseases including
heart, immological and psychiatric diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         507 ctcagtctcssaggaaaaaagacagggagcaaaggacaagaaatacgtctgg 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 0.5%; Score 15.2; DB 22; Langth 60; Local Similarity 65.7%; Predi No. 3.4ev0; 3.4ev0; etc. 3.6; Conservative 0; Mismatches 18; Indels is 3.
                                                                                                                                                                                        Human G-protein subunit Sbeta3 intron 9 DNA fragment #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 60 BP: 6 A; 11 C; 6 G; 37 T; 0 other;
4529 tarttacataaagactgtgctgaagaagcag 4558
                           37 CANTIGGARAACIACIGIGCITAGACGCAG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure: Page 3; 14pp; German.
                                                                    Best Loca
Matches
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This invention describes a novel method to detect N-terminal pro-brain nattiratetic privide (BNP) in a sample using two antibodies, that recognize distriction elitopes of the N-terminal pro-BNP. The method can be used for disquesting heart insufficiency. The recognizant in N-terminal pro-BNP is used for disquesting heart insufficiency. The recombinant in the useful as a standard in a method to detect N-terminal pro-BNP and also for production of antibodies against N-terminal pro-BNP. This sequence represents a primer used in the cloining of recombinant recomminal pro-BNP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1778 agggggcctgctgatgaagcagiactaccagtccatgctgcaggaggtcctgy4ggact 1837 | 178 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 179 | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene signature: messenyur RNA, mRNA: relative abundancu: frequency:
Furan: closing: mepping: vww.biseed library: diagnosis; detection;
ccll typing: abnormal ce:| lunction: ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oucry Match 0.5%; Score 25.2; DB 21; Length 70; Best Local Similarity b2.5%; Pred; No. 3.78+03. Metches 39, Conseavative C; Mismatches 23, Indets (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 70 BF, 10 A; 19 C; 21 G; 20 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT22066 Standard; cDNA to mRNA; 89 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human gene signature HUMGS03531.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-AUG-1996 (first, chtry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo saptens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09514772-A1.
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AAA71554 1D AAA71554 standard; DNA: 70 BP. XX XX NC AAA71554: XX

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The present sequence represents a PCR nutagenesis primer used to mutagenise the merk coding sequence derived from transposon Tn11, to adapt it for plant expressibility. The nucleic acid molecule produced is useful for producing transpenic plants that are resistant to toxic heavy netals (especially mercury) and so can be used remediate and/or revegetate contaminated areas. The becretial merk gene is derived from the transposon Tn11, which was originally isolated from the Incompatibility Group IncFII resistance plasmid NR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3026 atgtcctgactaatgtgagagtggtagaggtbcaayacccaggtgggcgactcaaggat 3085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 hagacccagetataggtgaagetgttaetgetgeatttegeatggaaggeattgaagtge 61
                                                                                                                                                                                                  DNA encoding marcuric ion reductase in plant-expressible form · for producing transgenic plants resistant to toxic heavy metals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 0.5%; Score 25.2; DB 18; Length 99; Best Local Similarity 54.3%; Pred. No. 4.78+03; Matches 51; Conservative 0; Mismatches 43; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 59 BP; 29 A; 21 C; 25 G: 24 T: 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3086 ttgattttctacaagcaattgaacctgcctttat 3119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Column 43-44; 52pp; English.
                                                                              (UYGE-) UNIV GEORGIA RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer 307-339S for In21 merA gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA228594 standard; DNA; 99 BP
                                         95US-0427097.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0427097.
  950S-0427097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9703-0878957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-DEC-1999 (first entry)
                                                                                                                        Summers AO;
                                                                                                                                                             WPI: 1997-470112/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
Transposon Tn2l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JUN-1997;
21-APR-1995;
                                       21-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-APR-1995;
                                                                                                                        Meagher RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5965796-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-oct-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA228594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           õ
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                                                                                                                                                                                                                                                                                                                                                                                             A single-stranded DNA (or its complementary strand or the corresp. comble-stranded DNA) which comprises one of the 7837 '62" sequences of given in AAT19001-72683 and which is able to hybridise to part of human genomic DNA. CDNA or mRNA is claimed. The GS (Gere Signature) sequences were obtained from a 'directed DDNA libraries prepared from various human tissues: synthesis of CDNA was initiated from the CS '-end of mRNA by using poly(T) as the sole primer. Since the 3'-outrans.stated conna hybridise with specific mRNA. Excl. in the different constructed conna hybridise with specific mRNA. Exch library is constructed conna st to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. waling primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e.9
                                                                                                                                                                                                                                                       Identifying gene signatures in 3'-directed human cDNA library - for disgnosis of abbormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.5%; Score 25.2; DB 16; Length 89; 62.9%; Pred. No. 4.4e+03; tive 0; Mismatches 23; indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Metal ion resistance; mercuric ion reductase; merk; marcury; toxic heavy metal: transgenic plant; mutagenic; bacterial; transposon; Tn2l; PCR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mercuric ion reductase merA PCH mutagenesis primer 307-339S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 89 BP; 39 A; 8 C; 15 G; 27 T: 0 other;
                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 1039; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT92244 standard; DNA; 99 BP.
                                         94WO-JP01916
                                                                            93JP-0355504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JAN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 62.9 Matches 39; Conservative
                                                                                                                                                                               Matsubara K, Okubo K;
                                                                                                                   (MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
                                                                                                                                                                                                                      WPI; 1995-206931/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transposon In21
                                       11-NOV-1994;
                                                                            12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4545 gt 4546
01-JUN-1995.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
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Organometal; resistance; transcription; translation; regulation; merA; transposon; fD21; merB; mercuric ion reductase; organomercury lysse: ss: transgenic plant; deloxification; metal compound; soil; sediment; priner; aquatic environment; bioremedation; contamination; PCR; amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Metal resistance sequences for producing transgenic plants .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYCE-) JNIV GEORGIA RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Summers AO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Meagher RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI: 1999-579950/49.
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16-SEP-1997

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                                                                              The invention relates to a nucleic acid molecule comprising a coding assumed to a nucleic acid molecule comprising a coding assumed an organometal resistance protein, which is operably in assumed and under the requisacry control of a marcuir of a control of a marcuir of a control of a contr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a primer used to generate a synthetic ofp gene by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Determining translational efficiency of codons in cells, comprising introducing synthetic constructs with reporter genes fused in frame to tandem repeats of the codon, and measuring expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3026 atgiccigacianalgigagagiggiagaggiacaagacccaggigggactcaaggal 3085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match

0.5%, Score 25.2; DB 20; Length 99;
Sect Local Similarity 54.3%; Pred. No. 4.7ev01.

Matches 51; Conservative 0; Mismatches 43; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 magacccagetataggtgaagetgttactgetgeatttegeatgguaggeattgaagtge 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Green fluorescent prolein; GFP; reporter gene; codon utilisation; translational efficiency; protein abundance; PCR primer: ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 99 BP; 29 A; 21 C: 25 G; 24 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3086 ttgattttctacaagcaattgaacctgcctttat 3119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Column 17-18; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1, Page 183, 193pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANA 3946 standard; DMA; 54 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GFP Leu(CTG)5 forward primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JAN-2000; 2000MO-AU00008.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-JAN-1999; 99AU-0008078.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UTQU ) UNIV QUEENSLAND. (SUNX/) SUN X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI: 2000-499118/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thou J. Frazer IH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W0230042215-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA73946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAA73946,C

AAAA73946,C

AAAA73946,C

AAAA73946,C

AAAA73946,C

AAAA73946,C

AAAA73946,C

AAAAA7346,C

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CCR amplification of a humanised gfp gene. A single artificial start codon followed by a streeth of five indentical acodons uses fused in frame codon followed by a streeth of five indentical acodons uses fused in frame. The amplified frament uses closed into the maintail an expression vector promisely by the contains XVV or and the CVV promoter, and was used in the promisely of a codon in a cell. The synchetic construct was introduced into toos is a codon in a cell. The synchetic construct was introduced into toos is a codon in a cell. The synchetic construct was introduced into toos is a codon in a cell. The synchetic constructs was made in which the gip gene is preceded to frame by a landem friend to the gip gene is preceded to frame by a landem friend to do triplete. Constructs he series covers the centre set of iscaccepting oddo triplete. Constructs higher procession of trainitional efficiency than their corresponding synonymous codons can be eight or replace the less preferred codons may then be used to replace the less preferred codons and the brother protein expression within undifferentiated epithelial cells such as COS-1 cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a single exon nucleic acid probe for makesuring human jene expression in a sangle derived from human foctal. Hiver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from luman (letal liver; the pressur sequence is a single exon nucleic acid human probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

0.55: Score 25; DD 21; Length 54:
Rest Local Smilarily 69:44: Pred. No. 3.6e-02;
Matches 34: Conservative 9; Hismatches 15: Indels D: Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome desived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4, SEQ ID NO 17996; 639pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human foetal liver single exon nucleic acid probe #17996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 54 BP; 9 A; 14 C; 20 G; 11 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Penn SG, Hanzel DK, Cher. W. Rank DR,
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25-MAY-2000; 2000:S-020456.

30-7W-2000; 2000:S-060840R.

03-ARC-2000; 2000:S-052386.

21-SEP-2000; 2000:S-0234687.

27-SEP-2000; 2000:S-023559.
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ID ABA69691 standard: DNA: 91 RP
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/published_pct_sequences.
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Sequence 91 BP; 28 A; 19 C; 13 G; 31 T; 0 other;

3815 acquattgasatattcgasgcatcaacaccccaatctggttcggtattttggtgtgg 3874 Gaps ö Query Natch 0.5%; Score 25; DB 22; Length 91; Best Local Similarity 61.5%; Pred. No. 5.1e+03; Matches 40; Conservative 0; Mismatches 25; Indels a

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67 AAGAAATTATAATGAAAGACTGTAAACACCCCAAATATTGTTGCTTATTATGGAAGCT 8

3875 agctc 3879

7 ATCTC 3 ò a

Human secreted protein 5' EST, SEQ ID NO: 16467.

Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosoma mapping; ss.

Duclert A, Giordano J;

New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cones and genomic DNAs that correspond to 5'ESTs and for disgnostic, forensic, gene therapy and chromosome mapping procedures

Isolated infectious chimeric parainfluenza virus (PIV), useful in an attenuated vaccine to elicits an immune response against one or more virus(es) selected from human PIV1 (HPIVI), HPIV2 and HPIV1.

Example 10; Page 150; 305pp; English.

Claim 1; SEQ ID 16467; 71pp + CD-ROM; English

The present sequence is one of a large number of S ESTs derived from manks emooding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5 ESTs were prepared from total human RNAs or polya+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from toliqued from the form the S's ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact S' ends and can therefore be used to obtain full length CDNAs and genomic DNNAs. S' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. expression and secretion vectors.

The present sequence for reverse PCR primer for respiratory syncytial vire present sequence for reverse PCR primer (RNY) A G gene insert is used with the forward PCR primer (AAS06929) in the construction of boving-humanPlV3-RSV chimeric viruses. The sequence is described in an invention relating to novel infectious chimeric parafilluanza viruses (PIVS). The virus comprises a mejor nucleocapsid protein (N), a nucleocapsid phosphoprotein (P), a large pulmerase protein (L), and a partial or complete PIV vector background genome, or antigenome combined with one or more berechologous gene(s) or genome segment(s) encoding one or more antigenic determinants of one or more heterologous pathogen(s) to form a chimeric genome or antigenome or human primer propose against one or more virus(es) selected from human PIVI (HPIVI), HPIVI and HPIVI and HPIVI he chimeric PIV may also elicit a polyapecific immune response against HPIVI and the second chimeric PIV elicits and munne response against HPIVI or HPIVI and where both the first and second chimeric PIVE elicits and immune response against HPIVI or HPIVI and where both the first and second chimeric PIVE elicits and immune response against HPIVI and immune response against HPIVI and immune response against HPIVI and HPIVI and where both the first and second chimeric PIVE elicits and second chimeric PIVE elicits and second chimeric PIVE elicits and prevent measiles and upper or lower respiratory tract infections

Sequence 77 BP; 27 A; 14 C; 15 G; 21 T; 0 other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hurphy BR. Collins PL, Schmidt AC, Durbin AP, Skiadopoulos MH:
Tao T:
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0.5%; Score 24.8; DB 21; Length 77:
60.3%; Pred. No. 5.2e+03;
iive 0; Mismatches 27; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reverse PCR primar for RSV A G gene insert.
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                                                                                                                                                                                                                                                                                                                                                                                      AASO66310 standard; DNA: 92 BP.

AASO6630.

XX
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AASO6930.

XX
I2-SEP-2001 (first entry)

XX
Infectious chimeric parainfluenza
WW incleacepsid phosphoprorectein; large
Nuclacocepsid phosphoprorectein; large
Numan PTV1: HPTV1: HPTV2: HPTV2: HPTV3:
XX
WAZO0142445-A2.

XX
HUMAN CESPITATOTY SYNCYLIAL VIRUS:
XX
WAZO0142445-A2.

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HUMAN CESPITATOTY SYNCYLIAL VIRUS:
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WAZO0142445-A2.

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HUMAN CESPITATOTY SYNCYLIAL VIRUS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human respiratory syncytial virus.
   Query Match 0.5
Best Local Similarity 60.3
Matches 41; Conservative
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The present sequence is one of a large number of 5' ESTs derived from anxiety and another of the bound as eccleduptocation. When the sequence is one of the sequence of the sequence is one of the sequence of the
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2 gamaatataaaaalactaancaaaqaaqtetgagglaactutggtaatattaaaactec 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human secreted protein 5' EST, SEQ ID No: 19516
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                                                                                                            1439 acoagetastggatggtteettycaaaggges 1476
                                                                                                                                                                                                                 52 angatttaatglaggaaatattattaaaggra 93
                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
AAC15541/c
ID AAC15541 standaid: cDKA: 94 BP.
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gene therapy; chromosome mapping; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 3.5%; Score 24.8; DB 22; Length 92; DB SEST Long 19.2; Length 92; BSEST Long SEST LANGE 18.2; Indels C; Caps Metches 38; Conservative C; Missatches 22; Indels C; Caps
                                                                                                     Sequence 92 BP; 20 A: 12 C; 26 G; 34 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human secreted protein 5' BST, SEQ ID NO: 15574.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 94 BP; 46 A; 9 C; 14 G; 25 T; 0 other;
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              particularly in young children.
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                                                                                                                                            Query Match 0.5%: Scole 24 8: DB 21; LengLh 94; Best Local Similarity 59:1%: Fred. No 64-40; Indels 0: Gaps Natches 39; Corservative 2: Mismetches 25; Indels 0: Gaps
Sequence 94 BF: 35 A: 10 C: 29 G; 16 T, 4 other:
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Query Mutch 0.5; Score 24.8; DB 21; Length 94; Bast Lonel Similarity 54.3%; Pred No. 5e-03; Indels 0; Caps Matches 50; Conservative 0; Mismatches 42; Indels 0; Caps

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AMES2008.

X. AMES208 standard: DNA: 71 BP.

X. AMES208.

X. AMES208.

X. AMES208.

X. AMES208.

X. AMES208.

X. AMES208.

Y. To SEP-1997 (first entry)

X. Margiorming: growth factor beta-1 binding ligand D 11.

X. Transforming: growth factor. beta-1. TGF-beta-1. binding ligand: dentification; SELEX; anti-microgenic; labbition. cell;

X. Transforming: growth factor beta-1 binding ligand D 11.

X. Transforming: growth factor beta-1 binding ligand D 11.

X. Transforming: growth factor beta-1 binding ligand: dentification; SELEX; anti-microgenic; labbition. cell;

X. M. Transforming: growth factor beta-1 binding ligand: dentification; SELEX; anti-microgenic; labbition.

X. M. Transforming: growth factor beta-1 binding: dentification; Synthetic.

X. M. Systematic Prolution of lagnosis; treatment; libroids: dentification; SELEX; asset dentification; Maintenance; The partitioned more dentification of nucleic acids was identificated by Steremitic Ecoles was contacted of the mature of nucleic calds was dentified by the dentified pathological conditions of the factor of the mat
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Query Match 0.5%; Score 24.6; DB 18; Length 71;
Best Local Similarity 65.5%; Pred. No. 5.7e+03;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps

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Search completed: May 29, 2002, 13:05:25 Job time: 9833 sec

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AR55745 G-10924. 6
AR346597 ch86b08. x
AR346999 ch86p09. x
AR346999 ch86p09. x
AR36669 AF49669
AR57427 m66609. x
AR57421 ch86p09. x
AR57421 ch86p09. x
AR57421 ch86p0. x
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us58102.rl Soares_thymus_ZNByT Hus musculus CDNA clone
THAGE.1381691 5', mRNA eequence.
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Mamaliar Bitheria Rodentia, Sciurognathi: Muxideo: Muthnew: Mus.
11. (Doses I (n. 95)
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2 AZ861698

C19910

AR54642

AL622095

AR57642

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AW5.6572

AR574215

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AR5743181

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B1443439

TA130801P
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      RESULT 1
AA990067
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JOURNAL
COMMENT
      May 28, 2002, 09:13:38; Search time 35:8.59 Suconds (Without allyments)
19141.135 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                             4990
i ctagaaqacttctccqatqa......ggtttattttaggaaagr.c 4990
                                   GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                13736207 segs. 6748477542 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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Maximum Match 1004
Listing first 45 summaries
                                                                                                                                   OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                       IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
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/organism="Mus musculus" /kinah="Cabbu.kG" /db_xxef="naxon:10090" /clone="IbAcE:1361691" /clone_11b="soare*_ihymus_2kb#T" /saz="male"

Source

FEATURES

AA99006 ua58202 r AA90064 ua5920 r A76708 u19390 r B906432 B106433 A136096 qy89409 x A136096 qy89409 x A15605 rq61010 r A1565 rq61010 r A1565 rq61010 r A1565 rq61010 r A1565 rq61010 r A1566 r A1766 r A1766

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95 70 70 70 83 10 95 95 95 93

Description

Score Match Length DB

Result No.

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Gaps

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Tumor Gene Index

(L Oppublished (1997)

Transon Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Email: cgapbs-remail.nih.gov

Trasue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Email: cgapbs-remail.nih.gov

Trasue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Arrayed by: Gree Lennon, Ph.D.

DNA Sequencing by: Washington University Gencem Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Conscortium/LLNL at:

www-bio.lini.gov/Dbrp/image.html

Insert Length: 785 Sid Error: 0.00

Seq primer: -400P from Globo

High quality sequence stop: 70.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anotes forgan: kidney: Vector: pT773D-Pac (Pharmacia) with a modified polylinker: Site_1: Not I: Site_2: Eco RI: Plasmid DNA from the normalized library NCI_CGAP_Kid5 was prepared, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The drivar was PCR-amplified cDNAs (clone pool of 5,000 clones made from the same library (cloneIDs 1123912-1135831, 1471369-1472903 and HAP Falima Bonaldo.
Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte ZhBM), pregnatu uterus whithy, and fetal heart NDHM194) were mixed, and as circles were made in vitro. Following HAP purification, this DNA was used as tracers in a subtractive hypitalization is sconsisted as tracers in a subtractive profitation of 5,000 clones made from the same 3 libraries. The pools of 5,000 clones made from the same 3 libraries. The pools 340488-345479, and 484488-88479."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A1767078 71 bp mRNA linear EST 21-DEC-1999 w192907.x1 NCI_CGAP_Kid12 Home sapiens cDNA clone IMAGE:2400828 3',
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Eukaryota, Hetazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Homanalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.
1. (bases 1 to 71)
MCT-CGAP http://www.ncbi.nlm.nlh.gov/nclogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone-INACE:400828*
/clone_lib="WCI_CGAP_Kid13"
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/lab_host="DH10b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.6%; Score 29; DB 9; Length 70; Best Local Similarity 71.7%; Pred. No. 1.4e+04; Matches 38; Conservative 0; Mismatches 15; Indels
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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16 c
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Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 70)

E 2 (bases 1 to 70)

E 3 (bases 1 to 70)

E 4 (bases 1 to 70)

Contact: Allson R.

Mashington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Far: 314 286 1800

Far:
                                                                                                       Anote-Vector: pt773D-pac (Pharmacia) with a modified polylinker; Site_1: Not I: Site_2: Eco Rr; ist strand CDNA was pitined with a Not I - oligo(d) primer [5' Corp. Site_2: Not I - oligo(d) primer [5' Corp. Site_2: Not I - oligo(d) primer [5'] double-stranded cohw was lighted to Eco RI adaptors 3'; double-stranded cohw was lighted to Eco RI adaptors and Eco RI sites of the modified pr773 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of cormalization, and was constructed by Bento Soares and M.Fatima Bonaldo.
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70 bp mRNA linear EST 08-AUG-1997

Aa44cl0.rl Scares_NhHMPu_S1 Homo sapiens cona clone IMAGE:823794 5'
similar to SW:NIM1_NEUCR P48479 PROTEIN KINASE NIM-1; , mRNA
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/clone_lib="Soares_NhHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Caps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 0.8% Score 39.8; DB 9; Length 55; Local Similarity 70.7%; Pred. No. 24; Local Similarity 70.7%; Pred. No. 24; Local Si; Conservative 0; Mismatches 22; Indeis
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/organism-"Homo saptens"
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               /tissue_type-"Thymus"
/dev_stage-"4 weeks"
/lab_host-"DH105"
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AA490364.1 GI:2219537
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CONA Library Arrayed by: Grey Leonou, Ph.D.
DRA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NGT-GRAP clore distribution information can be
found through the I.M.A.G.E. Consortium/LNNL at:
Why.bio.lini.gov/bop/langed/mayo.html
Insert Length: 1559 Sed Error: 0.00
Seq primer: -40UP from Gibso
High quality sequence stop: 76
Localion/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B1722285 94 bp mRNA linear EST 30-JUL-2001 XX15a08.y3 Parastronqyloides trichosuri fu pAMP1 vl Chiapelli MCCarter Parastrongyloides trichosuri cDNA 5', mRNA sequence. B122285
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Parastrongyloidus trithosuri.
Bukaryota: Macayoa Mematoda: Chromadorea: Rhahdilidu:
Baragrolainoidus. Sizongyloididus; Parastrongyloidus.
1 (basas: Lo 94)
McCarter.j., Olitton.S., Chiapolii, B., Papo, D., Martin.J., Wylle.T., Dante.M., Millier, L., Kucaba, T., Theising, B., Bowers, Y.
Homo sapiens
Eukarycka, Metazoa: Chordata: Craniata: Verlehrata; Fute:eostomi;
Mammalia: Entheria Primates: Catarrhini: Hominides: Homo.
1 (bases 1 to 81)
WI/NINDS-CAP http://www.ncbl.nlm.nlh.gov/nchcgap.
1 Disorders and Stroke, Biali Timor Genume Anatomy Project
(CAP/PRCAP). Trace Gene Index
Unpublished (1998)
Contact: Rober: Straubecy, Ph.D.
Email: capabs-refmail.nlh.gov
Email: capabs-refmail.nlh.gov
Tissue Procurement: David N. Lauls, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O; Caps
                                                                                                                                                                                                                                                               CONA Library Preparation: M. Bento Soares, Ph.D., M. Falima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               // Organism "Nomo sapiens"
// Ab ref "taxon: 966"
// Chome "! MAGE: 2019; 185 -
// Lissuc_Lype" anaplastin oligodendrogliome"
// 10a_host-'DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.6%; Score 27.8; DB 9; Length 83; 59.5%; Pred. No. 3e+04; tive 0; Mismatches 32; Indels
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DEFINITION qy99d09.x1 NCI_CGAP_Brn25 Homo sapiens CDNA clone IMAGE:2019185 3',
MRNA sequence.
ACCESSION AI360096
AI360096.1 GI:4111717
                                                                                                                                                                                                                                                                                             BJ063432 HIRB McChil normalized Xenopus tailbud inbrary Xenopus lavofatta cDNA clone XL076el3 5', mRNA Sequence.
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    (bases 1 to 83)
    Kitayama.A., Teresaka.C., Mochil.M., Ueno.N., Shin-i.T. and Kchara

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Amphlais Butaschia; Anura; Hesobatrachia; Pipoiden; Pipidae;
Kenopodinae; Kenopus;
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                                     0: Gaps
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/db_xref-"taxon:8355"
/clone="XLO'fell"
/clone="XLO'fell"
Liptary
Libear
Obery Match:

Best Local Similarity 64.2%; Pred. No. 1.78+040.

MacChes 43; Conservative 0: Mismatches 24; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Tadasu Shin-1
Center For Genetic Resource Information
Mational Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
78:: 81559-81-6855
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/dev_stage="stage 25"
15 a ll c ll g 42 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Expressed genes in X. laevis embryo Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: tshinifgenes.nig.ac.jp.
                                                                                                                                                                                                                                                                                                                                                            BJ063432,1 GI:17424723
                                                                                                                                                                                                                                                                                                                                                                                                                      African clawed frog.
Xenopus laevis
                                                                                                                                                      Oy 3145 ttgagtt 3151
                                                                                                                                                                                              62 TICATIT 68
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TITLE JOURNAL COMMENT

PEATURES

us-09-676-436-3.szlm100.rst

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91 bp mRNA linear EST 17-MAR-1995
946.4010.rl Soares fetal liver spleen iNFLS Homo septens cDNA clone
INAGE:112723 5' similar to 9b:X55446B_rnal 14-3-3 PROTEIN THFTA
(HUMAN); mRNA sequence.
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1 (bases 1 to 91)
Hillier.L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Kriftin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Materston,R., Williamson,A., Wohldmann,P. and Wilson,R.
Waterston, R.

The WashUr-HHMI Mouse EST Project
Unpublished (1996)

Contact: Marra M/House EST Project
WashUr-HHMI Mouse EST Project
The 13 14 286 1800
Fax: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1810
Fax
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq priner: -28M13 rev2 from Amersham
High quality sequence stop: 1.
Location/Qualiflers
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/clone-"TMAGE:583214"
/clone-llb-"Soares_thymus_2NDMT"
/sex-"male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .100.
/organism="Mus musculus"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                  The Mashington Univ. Nematode EST Project, 1999
Unpublished (1999)
Contact: MicCater of the Mashington University School of Medicine
The Mashington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 31
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The library was constructed by Brandi Chiapelli and Dr.
James McCarter at Washington University, St. Louis. The
CDNA was made by using Dynabead oilgo-dr priming (Dynab
FCR based library using a modified protocol from the
SMART PCR CDNA Syrthesis Kit from Clontech. Directionally
cloned into the UDG sites of pAMP1. Nemtodes were
provided by Dr. Warwick Grant of Agnearch, New Zealand
(warwick grant@agnesearch.co.nz).*

(warwick grant@agnesearch.co.nz).*
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Fukaryota: Metazos; Chordata; Craniata: Vartebrata; EuteleosLomi;

Mammalia: Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Nus.

1 (Dases I to 100)

Marra, M. Millier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Gelsel, S., Kucaba, T., Lacy, M., Tan, F., Underwood, K., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Milson, R. and
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             Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvill, R.,
Ronnody, S., Maguire, L., Beck, C., Underwood, W., Steptoe
M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S.,
Shin, T., Jackson, X., Cardenas, M., McCann, R., Waterston, R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.64; Score 27.8; DB 10; Length 94; Best Local Similarity 62.04; Pred. No. 3.1e+04; Matches 44; Condervative 0; Mismatches 27; Indels 0
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õ g ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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/ corganism* Homo saptens*
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COMM Library Progration: Devid B. Krizman, Ph.D.
COMM Library Arayed by: Gros Lannow, Ph. D.
COMM Library Arayed by: Gros Lannow, Ph. D.
DNA Sequenching by: Mashington University Genome Sequencing Contection distribution: Wil-CGNP clone distribution: information can be cover distribution: Wil-CGNP clone distribution: information can be owned through the LH.A.G.E. Consortium/LIML at:
Word-bio.Lihr.gov/2bepr/masqc.ham.
Insert length: 177 Sed Error: 0.00
Seq primer: 4(07) Fed. From Amersham.
Location/Qualifiers
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Expression map of the C.elegans genome
Uppublished (1996)
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/dp.ref**taxon:(219*
/clone=:by*Yulk Mohra unpublished CDMN*
/sex=*hermaphrodite, male*
/tissue_type=**Whole animal*
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Location/Qualifiers
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4444 Forest Park Parkway, Box 850., St. Louis, WO 51:08
4444 Forest Park Parkway, Box 850., St. Louis, WO 51:08
4444 Forest Park Parkway, Box 850., St. Louis, WO 51:08

Fax: 314 286 1800

Enail: selevation.wustl.edu

Insert Size: 715

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Mish quality sequence stris: 1 High quality sequence stops: 1

Forest Mish 10 or further information incortain (incottange lility)

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Location/Qualifiers
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/clone_ibb*Scares retal liver spleen INPLS*
/clone_ibb*Scares retal liver spleen INPLS*
/clone_ibb*Scares retal liver spleen in Catalians*
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AIGO4864 AIGO486 CDM COMPANA COMPA
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Bukaryota Metatoda Chordata; Craniata, Vertebrata; Eutelecstomi;

Manalia; Eutheria: Primates; Catarrinini, Hominidae, Homo.

1 (bases 1 to 90)

REI-CGAP Inter-//www.ncbi.nim.nih.gov/nclogap.

Mational Caneer Institute, Cancer Genome Anatomy Project (CGAP).
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Industrial (1997)
Contact: Nobert Strauberg, Ph.D.
Contact: Robert Strauberg, Ph.D.
Tissue Procurement: Wonkes Brown, M.D., Kilse Kchn, M.D., Michacl.
R. Emmert-Buck, M.D., Ph.D.
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54.4%; Pred. No. 3.98+04;
ative 0; Mismatches 36; Indels 0
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/db_xref="taxon:9606"
                 The MashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
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BASE COUNT

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Eukaryote, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi:
Mammalla: Eukheria; Rodentia; Sciurognathi; Muridae; Musnalla: Eutheria; Rodentia; Sciurognathi; Muridae; Musnalla: I (bases) I to 81)

NIH MGC http://mgc.ncl.nih.gov/.

NIH MGC http://mgc.ncl.nih.gov/.

NIH MGC http://mgc.ncl.nih.gov/.

Nutional institutes of Health, Mammallan Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg. Ph.D.

Contact: Robe
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                                                                                                                                                                 BEI01685 82 bp mRNA linear EST 19-OCT-2000 601753418F1 NCI_CGAP_Maml Mus musculus cDNA clone IMAGE:3980885 5',
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Mus musculus
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
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/clone="INAGE:3980885"
/clone=lib="MCI_cGAP_Mam.1
/clone_lib="MCI_cGAP_Mam.1
/dev_stage="10 months, virgin"
/lab_host="DH10R"
                                                                                                                                                                                                                                                                                        BF101686.1 GI:10884212
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En Marmalla: Entheria: Rodentia; Sciurognathi; Muridae; Musinae; Mus. 1 (bases 1 to 61)

En Mithonal Institutes of Health, Mammallan Gene Collection (MGC)

En Mithonal Institutes of Health, Mammallan Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Enail: Gapbs-remail.inh.gov

Tissue Procurement: Jeffrey Green M.D.

CONA Library Preparation: Life Technologies, Inc.

CONA Library Arrayed Dy: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing Dy: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:

http://image.llnl.gov

High quality sequence stop: 81.
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/strain="FVB/N"
/db_xref="taxon:10090"
/clone="inche:737010fe;
/sex="fena.e, virgin"
/tisus=Lype="infiltrating ductal carcinoms"
/lab_host="DH108"
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/dev_stage="varied"
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NRT Blochemistry.

I Pl Phoba S. Mandouhi.

HMT Blochemistry.

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Schellechagry.R., Schelboo.M., Ten.P., Underwood,R., Morote.B.,
Wateraton,R., Wylie,T., Lennon,G., Soakes,B., Wilson,R. and
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Email: W-Saber@FRCU.EUN.DC
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I. 95
Organism="Schistosoma mansoni"
(Organism="Schistosoma mansoni"
(Atain="Egyptian"
(Alba.host="Exon.6183"
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(Alba.host="E. coli IX Bluda"
(Alba.host="E. coli IX Bluda"
(Anote="Vector: pBluescript II Sk+: Site_]: EcoRl; Site_2: Nhol; makh was purified from adult couples of S. mansoni.
CPNA was constructed and cloned simultaneously using vector prining with the pBluescript II Sk+ vector. CDNA was directionally synthesized from the EcoRl site in the vector to the Nhol sites 39 t.
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Matches 45; Conservative 0; Mismatches 31; Indels 0; Gaps ò

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5: /cqn2_E/ptodata/1/ina/ba_COMB.seq:*

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1100 WHAEK: 33.7 1CATION INFORMATIC E: 212-867-0123 212-87-0123 POR SEQ ID NO: 4: MARCTRISTICS: 100 base pairs voleto acid WESS: 3inie	; NAME: Lambiris, Elias J.		
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TELEPHONE 212-867-0123 TELEPAR: 212-987-9655 THEAPLAR: 212-987-655 THEAPLAR: 212-987-655 THEAPLAR: 100 No. 4. TYPE: NO. 100 No. 6. TYPE: NO. 100 Lose pairs TYPE: No. 100 Lose pairs TRANDENNESS: single MOLECULE TYPE: DNA	; TELECOMMUNICATION INFORMATION:		
THERMAN: 212-878-9655 THERMAN: AND	: TELEPHONE: 212-867-0123		
INFORMATION POR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 100 base pairs STRANBEDNUSS: ainjle TOPOLOGY: 1 near MOLECULE TYPE: DNA US-08-400-225-4	; TELEFAX: 212-878-9655		
: SFOURMER CHARACTRRISTCS: I EDMOTH 100 base pairs TOPTO: noteled earls STRANDENESS single TOPPOLOTY: 1 nest WOLDCULE TYPE: DNA	; INFORMATION FOR SEQ ID NO: 4:		
: LEWITH: 100 base gairs : TYPE: notelected : STRANDENESS: angle : TOPOLOGY: 1 near : MOLECULE TYPE: DNA 35.08+400-256-4	; SPOUFNCE CHARACTERISTICS:		
; TYPE: nucleto ecid : STANDLOXY: : TOPOLOXY: 11near : MOLECULE TYPE: DNA US-08-400-22C	: LENGTH: 100 base pairs		
: STANDEDNESS: single : TOPOLOGS: Innear : MOLECULE TYPE: DNA US-08-400-256-4	; TYPE: nucleic acid		
: TOPOLOGY: 11near : MOLECULE TYPE: DNA US-08-400-225-4	STRANDEDNESS single		
YPE:	; TOPOLOGY: linear		
US-08-400-256-4			
	JS-08-400-256-4		
		25: Ja 1: Dengen 100;	
	DOLOGI BEIVE	. No. 0.18102) temptobes 40: Indels D:	80.00
5.5%; SCOIR 25; SB 1; Length 100; Similarity 55.6%; Pred, No. 6.16+02; Dength 100; Conservative 0; Mismarches 40; Indels 0;			

Application of the control of the co

Sequence seq

US-08-400-126-4
US-08-427-097-5
US-08-427-097-5
US-08-427-097-5
US-08-427-097-5
US-08-427-097-5
US-09-407-178-7
US-09-407-178-7
US-09-407-178-7
US-09-407-178-7
US-09-407-178-7
US-08-407-178-7

0 0 0 0 0 0

Description

Length

Query Match

Score

4469 aagaatgaageetagtagaatatggaettggaaaattetettaatemetactgtatgtaa 4528

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMMUTER: IBM FC COMPALIALE
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA: 21-APR-1995
CLASSIFICATION NUMBER: US/08/427,097
FILING DATE: 21-APR-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INPORMATION:
REGISTRATION UNMBER: 33.878
REFERENCE/DOCKET WINBER: 4C-94
TELECOMMUNICATION INFORMATION:
TELEFRAM: (303) 499-8089
INFORMATION FOR SEQ. 1D NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 base pairs
TYPE: nuclelc acid
                APPLICANT: Meagher, Richard B.
APPLICANT: Sommers, Anne O.
TITLE OF INVENTION: Hetal Resistance Sequences and
TITLE OF INVENTION: Transgenic Plants
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                    ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
NOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-878-957-5
; Sequence 5, Application US/08878957
; Patent No. 5965796
GENERAL INFORMATION:
APPLICANT: Meaghe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 80303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
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                                                                                                                                                                                                                                                                                                                                          Sequence 4. Application US/08975365
Patent No. 6011007
GENERAL INFORMATION:
APPLICANT: Halstrom, John
APPLICANT: Johnsen, John
APPLICANT: Andersen, John
APPLICANT: Andersen, John
APPLICANT: Andersen, John
APPLICANT: Andersen, John
APPLICANT: Acklarsen, John
APPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 AAGTCTGACGACGCTAAGGGTATCGTTGAACAATGTTGTACTTCTATCTGTTGTTAC 38
    Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
STATE: New York
COUNTRY: United States of America
LIP: 1014-6401
COMPUTER READABLE FORM:
WEDJUM TYPE: FLORPY disk
COMPUTER: IBM PC COMPATIble
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PareantIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

0.5%; Score 26; CB 3; CBest Local Similarity 55.6%; Pred. No. 6.18+02; Matches 50; Conservative 0; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/400,256
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: LAMBITIS, Elias J.
REGISTRATION NUMBER: 33,728
REFRENCE/DOCKET NUMBER: 3965,220-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4529 tatttacataaagactgtgctgagaagcag 4558
                                                                                                     37 CAATTGGAAAACTACTGTGCTTAGACGCAG 8
                                                                                                                                                                           37 CANTIGGAAACTACTGTGCTTAGACGCAC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/08427097
Patent No. 5658294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 100 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                         RESCLT 2
US-08-975-365-4/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
US-08-427-097-5
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3026 atetectgaetaaatgigagagtggtagaggtacaagaeceaggtgggegaeteaaggat 3085
                                                                                                                                                       Ouery Match 0.5%; Score 25.2; DB 1; Length 99; Rest Local Similarity 54.3%; Pred. No. 18+03; Matches 51; Conservative 0; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Weagher, Richard B.
APPLICANT: Weagher, Richard B.
APPLICANT: Summers, Anne O.
TITLE OF INVENTION: Metal Resistance Sequences and TITLE OF INVENTION: Transpenic Plants
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sulliven, P.C.
STREET: 3370 Manhattan Circle, Suite 201
CITY: Boilder
STREET: Colorado
                                                                                                                                                                                                                                   Oy 3086 ttgattttctacaagcaattgaacctgcctttat 3119
                                                                                                                                                                                                                                                                     62 GIGAGCATACTCAAGCAAGCCAAGTTGCCTATAT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U
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: inear
: MOLECULE TYPE: DNA
US-08-458-423A-78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oubry Match 99:

0.54; Scorc 25.2; DB 2; Length 99:
Best Local Similarity 54.34; Pred. No. (1e-05);
Matches 51; Conservative 0; Mishatches 43: Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 ANGACCCACCATAGGGGAAGGTGTTACTGCATTGCGCATTGCATGGAAGGCATTGAAGTGC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPRY: USA
ZIP: 00111
COMPUTER READABLE FORM:
HEDTUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Worlderfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 15,08/458,423A
FILING DATE: 2JUNE-1995
CLASSIFICATION: 556
    COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
CONFUTER: IMP PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PREVENTIN RELEASE #1.0, Version #1.30
CORRENT APPLICATION NOTE:
APPLICATION NUMBER: US/OB/878.957
FILTHG DATE: 19-10H-1997
FILTHG DATE: 1-APPLICATION NOTE: 31-APPLICATION NUMBER: 31-878
REGISTRATION NUMBER: 31-878
REGISTRATION NUMBER: 31-878
REFERENCE/DOCKET NUMBER: 31-878
REFERENCE/DOCKET NUMBER: 31-878
TELEPROME: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5

GG-08-128-78/C

GG-08-128-78/C

Sequence 78, Application US/08458423A

Patent No. 5731140+

GENERAL INFORMATION:

APPLICANT: PENELOPE J. TOOTHAAN

APPLICANT: LARRY GOLD

TITLE OF INVENTION: ACID LIGANDS AND INHIBITORS

TITLE OF INVENTION: ACID LIGANDS AND INHIBITORS

CORRESPONDED ADDRESSEE: SMANSON BAG BATASCHU, L.L.C.

ADDRESSEE: SMANSON BAG BATASCHU, L.L.C.

STREET: 8400 Eact Prentice Avenue, Sulte 4200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3086 ttgattttctacaaqcaattgaacctgcctttat 3119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 GTGAGCATACTCAAGCAAGCCAAGTTGCCTATAT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEG 1D NO: 5:
SEQUENCE CHRRACTERISTICS:
LENGTH: 99 base pairs
TYPE: nucleic acid
SYRANDEDNESS: aingle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 8400 Eas
CIfY: Denver
STATE: Colorado
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Ouery Match: 0.5%: Score 24.6; DB 1, Length 71; Best Local Similarity 65.5%; Pred. No. 1.2e+03; Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps
                                                                                                                                                                                                                          RESULT 6
CS-08-458-78-78-78
CS-08-458-458-78-78
CS-08-458-458-73-14-4
CS-08-458-458-73-14-4
CSBEALL INFORMATION:
CSBEALL INFORMATION:
CSBEALL INFORMATION:
CSBEALL INFORMATION:
CSBEAL LANT STEER RINGOLST
TITLE OF INVERTION:
CORRESS:
CORRESS:
CORRESS:
CORRESS:
CORRESS:
CORRESS:
CORRESS:
CORRESS:
COUNTRY:
COUNTRY:
COUNTRY:
COUNTRY:
COUNTRY:
CONTRY:
CO
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us-09-676-436-3.szlm100.rni

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3958 gaacatgtgattaggctgtattnaaagcagatcaccattgcgatcaacgtcctcc 4012
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PCT-USSG-08014-78/C

SEQUENCE 79, APPLICATION PC/TUSSG-08014

SEQUENCE 78, APPLICATION:

APPLICANT: LARRY GOLD; NEBOJSA JANJIC; STEVEN RINGGUIST;

APPLICANT: PRERAFICE PERELOPE J. TOOTHHAN

TITLE OF INVENTION: LIGAMES TO TRANSPORTING GROWTH

TITLE OF INVENTION: LIGAMES TO TRANSPORTING GROWTH

TITLE OF INVENTION: GROWTH FACTOR (TGF ), PLATELET-DERIVED

TITLE OF INVENTION: KEROTINOCKTE GROWTH FACTOR (NIGHT)

HUMBER OF SEQUENCES: 304

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.5%; Score 24.6; DB 4; Length 71; 65.5%; Pred. No. 1.2e+03; Live 0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER REGABLE FORM:
MEDION TYPE: DISKetter, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTMARE: WGOTGEFFCH. 6.1
CURRENT APPLICATION DATA.
APPLICATION NUMBER: PCT/US56/08014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Swanson & Bratschun, L.L.C. STREET: 8400 E. Prentice Avenue, Suite 200 CITY: Englewood STATE: Colorado
           PRICING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/46,591
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,725
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/419,783
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/618,693
FILING DATE: 20-MARCH-1996
ATTORNEY/ARD INFORMATION:
NAME: BATTY J. SWANGON
REGISTRATION NUMBER: 33.215
REFRERENCE/DOCKET NUMBER:
TELEPHONE: (303) 793-333
TELEPHONE: (303) 793-333
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 71 DASE PAIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458.423
FILING DATE: 02-3UNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,424
FILING DATE: 02-JUNE-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V.J.
Best Local Similarity 65.51
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
HOLECULE TYPE: DNA
US-08-973-124-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 80111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oucry Match 0.5%; Score 24.6; DB 1; Length 71: Best Local Similarity 65.5%; Pred. No. 1.2e+03; Matches 36; Conservative 0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette, 3.5 inch, 1.44 Mb storage
COMPUTER: TBM competible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,124
FILING DATE:
CLASSIFICATION NUMBER: US/08/973,124
FILING DATE: 30-MAY-1996
PRIOR DATE: 30-MAY-1996
PRIOR DATE: 08-458,423
FILING DATE: 02-JUNE-1995
FRIOR DATE: 02-JUNE-1995
FRIOR DATE: 02-JUNE-1995
FRIOR DATE: 02-JUNE-1995
PRIOR DATE: 03-JUNE-1995
PRIOR DATE: 03-JUNE-1995
PRIOR DATE: 03-JUNE-1995
PRIOR DATE: 03-JUNE-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-973-124-78/C
Sequence 78, Application US/08973124
Sequence 78, Application US/08973124
Patent No. 6207816
GENERAL INFORMATION:
APPLICANT: LARRY GOLD et al.
TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE
TITLE OF INVENTION: LIGANDS TO GROWTH
TITLE OF INVENTION: FACTORS
NUMBER OF SEQUENCES:
ADDRESSEE: SWANSON & Bratschun, L.L.C.
STREET: BAGO E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
FILING DATE: 21-OCTOBER-1992
FILING DATE: 21-OCTOBER-1993
APPLICATION NUMBER: 06/11, 991
FILING DATE: 8-SEPTEMBER-1993
PRIOR APPLICATION DATA: 07/931, 473
FILING DATE: 17-AUGUST-1993
APPLICATION WUMBER: 07/931, 473
FILING DATE: 17-AUGUST-1992
APPONENT/ACRET INCOMATION: NAME: DIANE B. MCCLGARD
REGISTRATION WUMBER: 33,960
REGISTRATION WUMBER: 33,960
REFERENCE/DOCKET WUMBER: NEX 34-75
TELECHOMONICATION INFORMATION:
TELECHOMONICATION INFORMATION:
TELECHOMONICATION INFORMATION:
TELECHOMONICATION INFORMATION:
SEQUENCE CINRACTERISTICS:
LENGTH: 71 base pairs
TYPE: OUTCLEC'S SINGLE
TYPE: OUTCLES: SINGLE
                                                                                                                                                                                                                                                                                                                                                                    NEX 34-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: 11near
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US-09-100-664A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9

RESULT 9

RESULT 9

S. 409-100-664A-5

IS 5640HOUTE 5. Application US/09100664A

Sequence 5. Application US/09100664A

PRESENT 100-6657129

APPLICANT: RIOSS, BRIAN

APPLICANT: RIOSS, BRIAN

APPLICANT: PRICE, JEFFREY

TITLE OF INVENTION: THERDOF

TITLE FO INVENTION: THERDOF

MUMBER OF SCHWENCE: 13

CORRESPONDENCE ADDRESS:

ADDRESSE: Alaubor 6 Jackson

STREET: All Nachemack

STATE: New Jersey

COMPITE: New Jersey

COMPUTE: USA

LIP: 07601

COMPUTE: W. Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER REDABLE FORM:
WEDIOM TIPE: Floppy disk
COMPUTER: Tay disk
COMPUTER: TAY COMPALIALE
OPERATIG STEER: PC-COS/M9-COS
SOFTWARE: PARENTER: PC-COS/M9-COS
SOFTWARE: PARENTER: PC-COS/M9-COS
CURRENT APPLICATION MARRER: DS/SOFY.100.664A
APPLICATION MARRER: DS/SOFY.100.664A
FILING DATE: 19-CUNH-1998
CLASSIFICATION HARBER: 19-CUNH-1998
ATCHER/AGENT INFORMATION:
NAME: JOCAGNT NEWARTION:
NAME: JOCAGNT NEWARTION:
REFERENCE/POCKET NUMBER: 26.742
REFERENCE/POCKET NUMBER: 26.742
PRIOR APPLICATION DATA:

APPLICATION MARER: 08/465,594
FILING DATE: 05-30NE-1995
PRIOR APPLICATION DATA: 1995
PRIOR APPLICATION DATA: 1995
FILING DATE: 05-30NE-1995
FILING DATE: 05-30NE-1995
FILING DATE: 07-30NE-1995
PRIOR APPLICATION DATA: 08/479,725
FILING DATE: 07-30NE-1995
PRIOR APPLICATION DATA: 08/479,783
FILING DATE: 07-30NE-1995
APPLICATION NUMBER: 08/479,783
FILING DATE: 20-30NECH-1996
ATTORNEY/ACENT INFORMATION: NAME: BALTY 2 SAMIGON
REGISTATION NUMBER: 33,215
FILING DATE: 07-3013
TELEFAX: (303) 793-333
TELEFAX: (303) 793-333
TELEFAX: 71 DASE PALITE
TYPE: NUMBER: ACID
ANNAMER: ACID
AND
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; TOPOLOGY: linear
; MOLECULE TYPE: DNA
PCT-US96-08014-78
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TELECOMBINITORIO REVORMETION:
TELECOMBINITORIO REVORMETION:
TELECOMBINITORIO REVORMETION:
TELECOMBINITORIO REVORMETION:
TELECOMBINITORIO REVORMETION:
TELECOMBINITORIO REVORMETION:
TOPOLOGI: 113321
TOPOLOGI: 1 linea
TOPOLOGI: 1 l
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
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US-08-95-365-9/C

US-08-975-365-9/C

Sequence 9, Application US/08975365

Patent No. 6011007

GENERAL INFORMATION

APPLICANT: Harbitom, John
APPLICANT: Harbitom, John
APPLICANT: Marksen, John
APPLICANT: Marksen, John
TITLE OF INVENTION: ACYLATED INSULIN

WUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6011007 No. 6011007th America, Inc.

STREET: 405 Lexington Avenue, 64th Floor

CITY: New York

STAMTE: New York

COUNTRY: United States of America

2.1P: 10174-6401
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Ouery Match 0.5%; Score 24.4; DB 1; Length 100; Best Local Similarity 54.4%; Pred, No. 1.7e+03; Matches 49; Conservative 0; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTE: IBH PC compatible
CORTUTE: IBH PC compatible
SOFTWARE: Petentin Release #1.0, Version #1.25
CURRENT APPLICATION DATE
TAPLICATION NUMBER: US/08/975,365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE LANDIAGE 13.728
REGISTRATION MUMBER: 33,728
REFERENCE/COCKET NUMBER: 3985.220-US
RELECONDUNICATION INFORMATION:
TELEPAONE: 212-867-0123
TELEPAONE: 212-867-0123
INFORMATION FOR SEQ 10 NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 base pairs
TYPE: nucleic acid
STRANBENESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/400,256
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA
US-D8-975-365-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /function= "synthetic storage protein
/product= "protein"
/gene= "ssp"
/stendard_name= "5.11.11.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.5%; Score 24; DB 1; Length 97; Best Local Similarity 58.3%; Pred. No. 2.2e+03; Matches 42; Conservative 0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                CORPART 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh Disk
COMPUTER: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 August 1991
ATORNEY/AGENT INFORMATION:
AMME: Linda Axamethy Floyd
REGISTRATION NUMBER: 33,692
FELEKOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ...CULUGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 97 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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us-09-676-436-3.szlml00.rni

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PROUT 14
PCT-US92-05412-54
FCT-US92-05412-54
FCT-US92-05412-54
FCT-US92-05412-54
FCT-USPACE STATE STAT
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Oust, Score 24: 08 5: Tength 97:
Marches 12: Conservative C: Mismarches 30: Indels 0: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function= "synthetic storage protein /product= "product="synthetin" /gene="sap" /standard name="5.11.11.5"
                                                                                                                                                                                                                                                                                                                                                                                      linear
: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOIGT: Inear
MOLECHIF TYPE: DNA (96007
ORIGINAL SOURCE:
STRAIN: B. COIL
TYPE: DHS
THREINE SOURCE:
CUCNE: 92-2
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OTHER INFORMATION:
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LOCATION: 3.88
OTHER INFORMATION: Attack protein
OTHER INFORMATION: Attack protein
OTHER INFORMATION: Attack protein
OTHER INFORMATION: /gene *ssp.
OTHER INFORMATION: /standard_name-
US-08-474-633A-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTE. U.S.A.

LIP. 1989

LIP. 1989

COMPUTER MADABLE FORM:
MEDIUM TYPE: FLOPPT DISK
COMPUTER. IBM PC COMPAT'BLE
OPERATING SYSTEM: PC-DOS/NS-POS
SOFTWARE: NICROSOFY MORD VERSION 2.0C
COMPUTERT APPLICATION ONTA:
APPLICATION WHOER: US/08/174,633A
                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: E. I. DU PONT DE NEMOURS
ADDRESSEE: AND COMPANY
STREET: 1007 MARKET STREET
CITY: MILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BB-1037-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:

CALS.FICKTON:

ATTORNEY AGENT INTORANTION:

NAME: BARBARA C. SIDERLA

REGISTRATION NUMBER: 30.684

REFERENCE/CONCEY NUMBER: BB-10.

TELEPRONE: 302-992-491

TELEFAN: 302-79-404

INTORANTION: 302-992-491

INTORANTION NO SEO ID NO: 63: 5EQUENCE CHARACTERISTICS:

LEANTH: 97 base pairs

IYPE: nuclet acid

STRANDEDNESS: GOUDLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomoración constituente const
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:: 68
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Matchés 42; Conservative C: Mismatches 30; Indels 0; Gaps Cy 1120 gaptacaggtyatiyacanagayatatathe D: Gaps Cy 1120 gaptacaggtyatiyacanagayatathe D: Lo Gaptacaggtyatiyacanagayatathe D: Lo Gaptacaggtyatiyacanagayatathe D: Lo Gaptacagayatathe D: Company Company
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GENERAL INCORANTION WOORDINGS A PRESENCE OF APPLICANT: Shary! Thompson TITLE OF INVENTION: WOOTIGL CALL OF CONTRICES.

GENERAL INCORMATION: MODIFICATION OF CTYPLIC SPLICE SILES IN AUGUSER OF SEQUENCES: 21 CORRESPONDERS.

GORRESPONDERS S.

GORRESP
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0; Gaps

Query Match 0.5%; Score 23.8; DB 1; Length 83; Best Local Similarity 72.1%; Prod. No. 2.3e+03; Matches 31; Conservative 0; Mismatches 12; Indels

Search completed: May 29, 2002, 12:56:56 Job time: 9665 sec